

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:21:13 ; Search time 214.344 Seconds  
(without alignments)  
684,218 Million cell updates/sec

Title: US-10-517-956-1

Perfect score: 1817  
Sequence: 1 METNFTPLNXYEVEVSYESA.....TNDTANASPPAETELQAM 351

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA Main:

- 1: /cgn2\_6/prodata/1/pubpaa/us07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/1/pubpaa/us08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/prodata/1/pubpaa/us09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/prodata/1/pubpaa/us10\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata/1/pubpaa/us10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/prodata/1/pubpaa/us11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1817	100.0	351	3	US-09-944-807-2	Sequence 2, Appl1
2	1817	100.0	351	4	US-10-225-567A-120	Sequence 120, App
3	1817	100.0	351	5	US-10-874-015-2	Sequence 2, Appl1
4	1817	100.0	351	5	US-10-482-029-263	Sequence 263, App
5	1817	100.0	351	5	US-10-509-715-2	Sequence 2, Appl1
6	1817	100.0	351	5	US-10-517-956-1	Sequence 1, Appl1
7	1811	99.7	351	3	US-09-826-509-501	Sequence 501, App
8	1811	99.7	351	5	US-10-925-095-501	Sequence 501, App
9	1420	78.2	351	5	US-10-517-956-12	Sequence 12, Appl
10	1419	78.1	351	5	US-10-517-956-12	Sequence 10, Appl
11	1327	73.0	581	5	US-10-505-486-118	Sequence 118, App
12	1318	72.5	353	4	US-10-225-567A-633	Sequence 633, App
13	1318	72.5	353	4	US-10-116-275-218	Sequence 218, App
14	1318	72.5	353	4	US-10-789-241-12	Sequence 12, Appl
15	1318	72.5	353	5	US-10-517-956-14	Sequence 14, Appl
16	1304	71.8	349	4	US-10-305-555-8	Sequence 8, Appl1
17	1250.5	68.8	350	4	US-10-325-567A-631	Sequence 631, App
18	1250.5	68.8	350	4	US-10-354-358-2	Sequence 2, Appl1
19	1244.5	68.5	350	3	US-09-826-509-499	Sequence 499, App
20	1244.5	68.5	350	5	US-10-925-095-499	Sequence 499, App
21	1243.5	68.4	351	3	US-09-893-512-16	Sequence 16, Appl
22	1243.5	68.4	351	5	US-10-799-736-16	Sequence 16, Appl
23	1174.5	64.6	354	3	US-09-867-569-11	Sequence 11, Appl
24	1174.5	64.6	354	4	US-10-218-574-11	Sequence 11, Appl
25	1174.5	64.6	354	5	US-10-984-898-11	Sequence 11, Appl
26	1157.5	63.7	343	3	US-09-879-017-2	Sequence 2, Appl1
27	1107.5	61.0	323	4	US-10-005-196-2	Sequence 2, Appl1

28	1107.5	61.0	323	4	US-10-026-937-2	Sequence 2, Appl1
29	554.5	30.5	356	4	US-10-251-385-246	Sequence 246, App
30	554	30.5	594	5	US-10-505-486-119	Sequence 119, App
31	553.5	30.5	342	4	US-10-226-102-4	Sequence 4, Appl1
32	553.5	30.5	342	4	US-10-407-079-4	Sequence 4, Appl1
33	553.5	30.5	356	4	US-10-226-102-2	Sequence 2, Appl1
34	553.5	30.5	356	4	US-10-226-102-17	Sequence 17, Appl
35	553.5	30.5	356	4	US-10-251-385-270	Sequence 270, App
36	553.5	30.5	356	4	US-10-225-567A-484	Sequence 484, App
37	553.5	30.5	356	4	US-10-407-079-2	Sequence 2, Appl1
38	553.5	30.5	356	4	US-10-407-079-17	Sequence 17, Appl
39	553.5	30.5	356	5	US-10-684-206-4	Sequence 4, Appl1
40	553.5	30.5	390	4	US-10-017-161-760	Sequence 760, App
41	542.5	29.9	477	3	US-09-892-206-2	Sequence 2, Appl1
42	542.5	29.9	477	4	US-10-764-649-10	Sequence 10, Appl
43	542.5	29.9	477	6	US-11-046-857-4	Sequence 4, Appl1
44	538.5	29.6	371	3	US-09-905-253A-4	Sequence 4, Appl1
45	538.5	29.6	371	4	US-10-201-187-4	Sequence 4, Appl1

## ALIGNMENTS

RESULT 1  
US-09-944-807-2  
Sequence 2, Application US/09944807  
Patent No. US20020119494A1  
GENERAL INFORMATION:  
APPLICANT: Boehringer Ingelheim Pharma KG  
TITLE OF INVENTION: Method for identifying substances which positively  
TITLE OF INVENTION: Influence inflammatory conditions of chronic  
TITLE OF INVENTION: Inflammatory airway diseases  
FILE REFERENCE: 082.00n  
CURRENT APPLICATION NUMBER: US/09/944,807  
CURRENT FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: UK 0021484.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 2  
LENGTH: 351  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-944-807-2

Query Match 100.0%; Score 1817; DB 3; Length 351;  
Best Local Similarity 100.0%; Pred. No. 2.9e-148; Indels 0; Gaps 0;  
Matches 351; Conservative 0; Mismatches 0;

QY	1	METNFTPLNXYEVEVSYESAGYTVLRILPLVVLGVTVFVLGNGLVIWVAGFRMTRTVY	60
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QY	61	TTCTYMLALADSPFTATLPLIVSNMAGKWPFWLCKLIHIVDINLFGSVFLIGFTA	120
DB	61	TTCTYMLALADSPFTATLPLIVSNMAGKWPFWLCKLIHIVDINLFGSVFLIGFTA	120
QY	121	LDRCTVLAHPWAQNRRTYSLAMKYVGPWIIALVITLVEPLFTVTIPNGDTCTPWF	180
DB	121	LDRCTVLAHPWAQNRRTYSLAMKYVGPWIIALVITLVEPLFTVTIPNGDTCTPWF	180
QY	181	ASWGTPBERLKVATMLTARGIIRVIGFSLPMSIVAICYGIIAKIKHKGMKISRP	240
DB	181	ASWGTPBERLKVATMLTARGIIRVIGFSLPMSIVAICYGIIAKIKHKGMKISRP	240
QY	241	RVLTAVVAFFTCWPFQVALLGVTLKEMLPYGRYKTIIDILVNFTSSLAFFNSCLNPM	300
DB	241	RVLTAVVAFFTCWPFQVALLGVTLKEMLPYGRYKTIIDILVNFTSSLAFFNSCLNPM	300
QY	301	LVPFVQDPRRLIHSLPTSLRALSEDSAPINDTANASPPAETELQAM 351	
DB	301	LVPFVQDPRRLIHSLPTSLRALSEDSAPINDTANASPPAETELQAM 351	

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RESULT 2
US-10-225-567A-120
; Sequence 120, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmet, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-120

Query Match      100.0%; Score 1817; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 2.9e-148;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEXEYEVESAGYTVLRILPLVVLGVTFLVGLNGLVIVWAGFRMTRTYT 60
DB 1 METNFTPLNEXEYEVESAGYTVLRILPLVVLGVTFLVGLNGLVIVWAGFRMTRTYT 60
QY 61 TICYNLALADSFATLPLPLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVFLIGFLA 120
DB 61 TICYNLALADSFATLPLPLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVFLIGFLA 120
QY 121 LDRICVLAHPVWAQNHRVSLAMKVI VGPWILALVTLPLVFLTTVTI PNGDTYCTENF 180
DB 121 LDRICVLAHPVWAQNHRVSLAMKVI VGPWILALVTLPLVFLTTVTI PNGDTYCTENF 180
QY 181 ASWGCTPEERLKVATITMLTARGIIRFVIGFSLPMSIVACGLIAAKIHKKGMIKSSRPL 240
DB 181 ASWGCTPEERLKVATITMLTARGIIRFVIGFSLPMSIVACGLIAAKIHKKGMIKSSRPL 240
QY 241 RVLTAVASFFICWPFQVALLGTWMLKEMLFYGRKXIIDLIVNPTSSIAFPNSCLNPM 300
DB 241 RVLTAVASFFICWPFQVALLGTWMLKEMLFYGRKXIIDLIVNPTSSIAFPNSCLNPM 300
QY 301 LVFVGQDFRERLIHSLPTSLERALSDESAPTNDTAANSASPATTELQAM 351
DB 301 LVFVGQDFRERLIHSLPTSLERALSDESAPTNDTAANSASPATTELQAM 351

RESULT 3
US-10-874-015-2
; Sequence 2, Application US/10874015
; Publication No. US20040253630A1
; GENERAL INFORMATION:
; APPLICANT: Jung, Birgit
; APPLICANT: Kraut, Norbert
; APPLICANT: Mueller, Stefan
; APPLICANT: Kistler, Barbara
; APPLICANT: Seither, Peter
; APPLICANT: Quast, Karsten
; APPLICANT: Welch, Andreas
; TITLE OF INVENTION: Method for identifying substances which positively
; TITLE OF INVENTION: Influence inflammatory conditions of chronic
; FILE REFERENCE: 1/1144-1-D1
; CURRENT APPLICATION NUMBER: US/10/874,015
; CURRENT FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
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NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-874-015-2

Query Match      100.0%; Score 1817; DB 5; Length 351;
Best Local Similarity 100.0%; Pred. No. 2.9e-148;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEXEYEVESAGYTVLRILPLVVLGVTFLVGLNGLVIVWAGFRMTRTYT 60
DB 1 METNFTPLNEXEYEVESAGYTVLRILPLVVLGVTFLVGLNGLVIVWAGFRMTRTYT 60
QY 61 TICYNLALADSFATLPLPLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVFLIGFLA 120
DB 61 TICYNLALADSFATLPLPLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVFLIGFLA 120
QY 121 LDRICVLAHPVWAQNHRVSLAMKVI VGPWILALVTLPLVFLTTVTI PNGDTYCTENF 180
DB 121 LDRICVLAHPVWAQNHRVSLAMKVI VGPWILALVTLPLVFLTTVTI PNGDTYCTENF 180
QY 181 ASWGCTPEERLKVATITMLTARGIIRFVIGFSLPMSIVACGLIAAKIHKKGMIKSSRPL 240
DB 181 ASWGCTPEERLKVATITMLTARGIIRFVIGFSLPMSIVACGLIAAKIHKKGMIKSSRPL 240
QY 241 RVLTAVASFFICWPFQVALLGTWMLKEMLFYGRKXIIDLIVNPTSSIAFPNSCLNPM 300
DB 241 RVLTAVASFFICWPFQVALLGTWMLKEMLFYGRKXIIDLIVNPTSSIAFPNSCLNPM 300
QY 301 LVFVGQDFRERLIHSLPTSLERALSDESAPTNDTAANSASPATTELQAM 351
DB 301 LVFVGQDFRERLIHSLPTSLERALSDESAPTNDTAANSASPATTELQAM 351

RESULT 4
US-10-482-029-263
; Sequence 263, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 263
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-263

Query Match      100.0%; Score 1817; DB 5; Length 351;
Best Local Similarity 100.0%; Pred. No. 2.9e-148;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEXEYEVESAGYTVLRILPLVVLGVTFLVGLNGLVIVWAGFRMTRTYT 60
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QY 61 TICYNLALADSFATLPLPLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVFLIGFLA 120
DB 61 TICYNLALADSFATLPLPLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVFLIGFLA 120
QY 121 LDRICVLAHPVWAQNHRVSLAMKVI VGPWILALVTLPLVFLTTVTI PNGDTYCTENF 180
DB 121 LDRICVLAHPVWAQNHRVSLAMKVI VGPWILALVTLPLVFLTTVTI PNGDTYCTENF 180
QY 181 ASWGCTPEERLKVATITMLTARGIIRFVIGFSLPMSIVACGLIAAKIHKKGMIKSSRPL 240
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Db 181 ASWGTEPERLKAITMTLARGIIRFYIGSLPMSIYALCYGLIAAKIHKKGMKISRPL 240  
Qy 241 RVLTAIVASFFICMPFPQVALIGTVMKEMLFYGYKXIIDIIVNPTSSIAFPNSCLNPM 300  
Db 241 RVLTAIVASFFICMPFPQVALIGTVMKEMLFYGYKXIIDIIVNPTSSIAFPNSCLNPM 300  
Qy 301 LYYFVGODFRERLIHSLPTSLERALSDESAFTNDTANASPPAETELQAM 351  
Db 301 LYYFVGODFRERLIHSLPTSLERALSDESAFTNDTANASPPAETELQAM 351

RESULT 5  
US-10-509-715-2

; Sequence 2, Application US/10509715  
; Publication No. US20050164305A1  
; GENERAL INFORMATION:  
; APPLICANT: Goiz, Stefan  
; APPLICANT: Bruggemeier, Ulf  
; APPLICANT: Geerts, Andreas  
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with  
; TITLE OF INVENTION: N-Formyl Peptide Receptor Like 1 (FPR1)  
; FILE REFERENCE: Le A 35 949  
; CURRENT APPLICATION NUMBER: US/10/509, 715  
; CURRENT FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER: PCT/EP03/02959  
; PRIOR FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: EP 02007291.4  
; PRIOR FILING DATE: 2002-04-03  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patentin Version 3.3  
; SEQ ID NO 2  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-509-715-2

Query Match 100.0%; Score 1817; DB 5; Length 351;  
Best Local Similarity 100.0%; Pred. No. 2.9e-148;  
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METNFTPLNBYEBSYBSAGYTVLRILPLVVLGTVFVLGVLNGVIVWAGFRMTRTYT 60  
Db 1 METNFTPLNBYEBSYBSAGYTVLRILPLVVLGTVFVLGVLNGVIVWAGFRMTRTYT 60  
Qy 61 TICYLNLALADFSFTATLPLPLIVSMAMGKMPGMPFLCKLIHIVVDINLFGSVFLIGFIA 120  
Db 61 TICYLNLALADFSFTATLPLPLIVSMAMGKMPGMPFLCKLIHIVVDINLFGSVFLIGFIA 120  
Qy 121 LDRICICLHPVMAQNHRVTSIAKVIIVGPMIALVLTLPVFLPTVTIIPNGDYCTCFNF 180  
Db 121 LDRICICLHPVMAQNHRVTSIAKVIIVGPMIALVLTLPVFLPTVTIIPNGDYCTCFNF 180  
Qy 121 LDRICICLHPVMAQNHRVTSIAKVIIVGPMIALVLTLPVFLPTVTIIPNGDYCTCFNF 180  
Db 121 LDRICICLHPVMAQNHRVTSIAKVIIVGPMIALVLTLPVFLPTVTIIPNGDYCTCFNF 180  
Qy 181 ASWGTEPERLKAITMTLARGIIRFYIGSLPMSIYALCYGLIAAKIHKKGMKISRPL 240  
Db 181 ASWGTEPERLKAITMTLARGIIRFYIGSLPMSIYALCYGLIAAKIHKKGMKISRPL 240  
Qy 241 RVLTAIVASFFICMPFPQVALIGTVMKEMLFYGYKXIIDIIVNPTSSIAFPNSCLNPM 300  
Db 241 RVLTAIVASFFICMPFPQVALIGTVMKEMLFYGYKXIIDIIVNPTSSIAFPNSCLNPM 300  
Qy 301 LYYFVGODFRERLIHSLPTSLERALSDESAFTNDTANASPPAETELQAM 351  
Db 301 LYYFVGODFRERLIHSLPTSLERALSDESAFTNDTANASPPAETELQAM 351

RESULT 6  
US-10-517-956-1

; Sequence 1, Application US/10517956  
; Publication No. US20050233326A1  
; GENERAL INFORMATION:  
; APPLICANT: Takeda Chemical Industries, Ltd.  
; TITLE OF INVENTION: Novel Screening Method  
; FILE REFERENCE: 3067WOOP

; CURRENT APPLICATION NUMBER: US/10/517, 956  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: JP 2002-173798  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: JP 2002-205470  
; PRIOR FILING DATE: 2002-07-15  
; NUMBER OF SEQ ID NOS: 24  
; SEQ ID NO 1  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Human  
US-10-517-956-1

Query Match 100.0%; Score 1817; DB 5; Length 351;  
Best Local Similarity 100.0%; Pred. No. 2.9e-148;  
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METNFTPLNBYEBSYBSAGYTVLRILPLVVLGTVFVLGVLNGVIVWAGFRMTRTYT 60  
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Db 61 TICYLNLALADFSFTATLPLPLIVSMAMGKMPGMPFLCKLIHIVVDINLFGSVFLIGFIA 120  
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Db 121 LDRICICLHPVMAQNHRVTSIAKVIIVGPMIALVLTLPVFLPTVTIIPNGDYCTCFNF 180  
Qy 181 ASWGTEPERLKAITMTLARGIIRFYIGSLPMSIYALCYGLIAAKIHKKGMKISRPL 240  
Db 181 ASWGTEPERLKAITMTLARGIIRFYIGSLPMSIYALCYGLIAAKIHKKGMKISRPL 240  
Qy 241 RVLTAIVASFFICMPFPQVALIGTVMKEMLFYGYKXIIDIIVNPTSSIAFPNSCLNPM 300  
Db 241 RVLTAIVASFFICMPFPQVALIGTVMKEMLFYGYKXIIDIIVNPTSSIAFPNSCLNPM 300  
Qy 301 LYYFVGODFRERLIHSLPTSLERALSDESAFTNDTANASPPAETELQAM 351  
Db 301 LYYFVGODFRERLIHSLPTSLERALSDESAFTNDTANASPPAETELQAM 351

RESULT 7  
US-09-826-509-501

; Sequence 501, Application US/09826509  
; Publication No. US20030204073A1  
; GENERAL INFORMATION:  
; APPLICANT: Lehmann-Bruhnsma, Karin  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G  
; TITLE OF INVENTION: Protein-coupled Receptors  
; FILE REFERENCE: ALEN-207  
; CURRENT APPLICATION NUMBER: US/09/826, 509  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/195, 747  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 09/170, 496  
; PRIOR FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 589  
; SOFTWARE: Patentin Version 2.1  
; SEQ ID NO 501  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-826-509-501

Query Match 99.7%; Score 1811; DB 3; Length 351;  
Best Local Similarity 99.7%; Pred. No. 9.6e-148;  
Matches 350; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 METNFTPLNBYEBSYBSAGYTVLRILPLVVLGTVFVLGVLNGVIVWAGFRMTRTYT 60  
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Db 61 TICYLNLALADSFATLPLPLIVSMAMGKMPGMPFLCKLIHIYVDINLFGSVPLIGFIA 120
Qy 121 LDRICICVLHPVMAQNHRVTSIAMKVIVGPMILAVLTPVPLFTVTITPNSGDTCTFNF 180
Db 121 LDRICICVLHPVMAQNHRVTSIAMKVIVGPMILAVLTPVPLFTVTITPNSGDTCTFNF 180
Qy 181 ASWGTPEERLKVATITMLTARGIIRFVIGFSLPMSIYACGLIAAKIHKKGMIKSSRPL 240
Db 181 ASWGTPEERLKVATITMLTARGIIRFVIGFSLPMSIYACGLIAAKIHKKGMIKSSRPL 240
Qy 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYKGYKIIDILVNPTSSIAFNSCLNPM 300
Db 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYKGYKIIDILVNPTSSIAFNSCLNPM 300
Qy 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPAPTNDTAANSAPPAETELQAM 351
Db 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPAPTNDTAANSAPPAETELQAM 351
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## RESULT 8

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US-10-925-095-501
; Sequence 501, Application US/10925095
; Publication No. US20050019840A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruhmann, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925, 095
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826, 509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195, 747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170, 496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 501
; LENGTH: 351
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-925-095-501
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Query Match 99.7%; Score 1811; DB 5; Length 351;

Best Local Similarity 99.7%; Pred. No. 9.6e-148;

Matches 350; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 METNFSPTLMEYEVSYESAGYTVLRILPLVLGVTFVLGVLGNGLVIVWAGFRMTRTVT 60
Qy 61 TICYLNLALADSFATLPLPLIVSMAMGKMPGMPFLCKLIHIYVDINLFGSVPLIGFIA 120
Db 61 TICYLNLALADSFATLPLPLIVSMAMGKMPGMPFLCKLIHIYVDINLFGSVPLIGFIA 120
Qy 121 LDRICICVLHPVMAQNHRVTSIAMKVIVGPMILAVLTPVPLFTVTITPNSGDTCTFNF 180
Db 121 LDRICICVLHPVMAQNHRVTSIAMKVIVGPMILAVLTPVPLFTVTITPNSGDTCTFNF 180
Qy 181 ASWGTPEERLKVATITMLTARGIIRFVIGFSLPMSIYACGLIAAKIHKKGMIKSSRPL 240
Db 181 ASWGTPEERLKVATITMLTARGIIRFVIGFSLPMSIYACGLIAAKIHKKGMIKSSRPL 240
Qy 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYKGYKIIDILVNPTSSIAFNSCLNPM 300
Db 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYKGYKIIDILVNPTSSIAFNSCLNPM 300
```

```
Qy 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPAPTNDTAANSAPPAETELQAM 351
Db 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPAPTNDTAANSAPPAETELQAM 351
```

## RESULT 9

```
US-10-517-956-12
; Sequence 12, Application US/10517956
; Publication No. US2005023326A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Novel Screening Method
; FILE REFERENCE: 3067WOOP
; CURRENT APPLICATION NUMBER: US/10/517, 956
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: JP 2002-173798
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: JP 2002-205470
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 12
; LENGTH: 351
; TYPE: PRN
; ORGANISM: Mouse
US-10-517-956-12
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Query Match 78.2%; Score 1420; DB 5; Length 351;

Best Local Similarity 76.3%; Pred. No. 4.9e-114;

Matches 267; Conservative 33; Mismatches 50; Indels 0; Gaps 0;

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Qy 1 METNFSPTLMEYEVSYESAGYTVLRILPLVLGVTFVLGVLGNGLVIVWAGFRMTRTVT 60
Db 1 MESNVSIHNGSEVVVYDDSTISRVMIISMVVVSITFFGVGNGLVIVWAGFRMTRTVT 60
Qy 61 TICYLNLALADSFATLPLPLIVSMAMGKMPGMPFLCKLIHIYVDINLFGSVPLIGFIA 120
Db 61 TICYLNLALADSFATLPLPLIVSMAMGKMPGMPFLCKLIHIYVDINLFGSVPLIGFIA 120
Qy 121 LDRICICVLHPVMAQNHRVTSIAMKVIVGPMILAVLTPVPLFTVTITPNSGDTCTFNF 180
Db 121 LDRICICVLHPVMAQNHRVTSIAMKVIVGPMILAVLTPVPLFTVTITPNSGDTCTFNF 180
Qy 181 ASWGTPEERLKVATITMLTARGIIRFVIGFSLPMSIYACGLIAAKIHKKGMIKSSRPL 240
Db 181 ASWGTPEERLKVATITMLTARGIIRFVIGFSLPMSIYACGLIAAKIHKKGMIKSSRPL 240
Qy 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYKGYKIIDILVNPTSSIAFNSCLNPM 300
Db 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYKGYKIIDILVNPTSSIAFNSCLNPM 300
Qy 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPAPTNDTAANSAPPAETELQAM 350
Db 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPAPTNDTAANSAPPAETELQAM 350
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## RESULT 10

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US-10-517-956-10
; Sequence 10, Application US/10517956
; Publication No. US2005023326A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Novel Screening Method
; FILE REFERENCE: 3067WOOP
; CURRENT APPLICATION NUMBER: US/10/517, 956
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: JP 2002-173798
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: JP 2002-205470
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 10
; LENGTH: 351
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; TYPE: PRT
; ORGANISM: Rat
US-10-517-956-10

```

Query Match	78.1%	Score 14.9	DB 5	Length 351
Best Local Similarity	74.9%	Pred. No. 6e-11.4		
Matches 263, Conservative	37	Mismatches	51	Indels 0; Gaps 0

Qy	1	MEINFSTPLANEVEESYBSAGVTVRIIRPLVVGTFPLGVLGNGVLVWVAGFPMSTVT	60
Qy	2	MEINFSTPLANEVEESYBSAGVTVRIIRPLVVGTFPLGVLGNGVLVWVAGFPMSTVT	60
Db	1	MEANYSIPLANSEVYVYDSTISRVLMLTLMVVLSTTFPLGVLGNGVLVWVAGFPMHTVT	60
Qy	61	TIICYNIALADSPFATLPEPLIVSNAMGEKMPFGMLCKLIHIVDINLFGSVELIGFIA	120
Qy	61	TIICYNIALADSPFATLPEPLIVSNAMGEKMPFGMLCKLIHIVDINLFGSVELIGFIA	120
Db	61	TIICYNIALADSPFATLPEPLIVSNAMGEKMPFGMLCKLIHIVDINLFGSVELIALIA	120
Qy	121	LDRICICVLHPWAQNHRITVSLAMKVI VGPWILATLVLPVLPFLTTVTIPNGDYCTENF	180
Qy	121	LDRICICVLHPWAQNHRITVSLAMKVI VGPWILATLVLPVLPFLTTVTIPNGDYCTENF	180
Db	121	LDRICICVLHPWAQNHRITVSLARKVVGPMILATLITLPFIEMTVARIPEGNYCTENF	180
Qy	181	ASWGGSIPBEERLKAVALTMTLARGIIRPVIGFSIPMSIYACGLIAAKHKMKKSRRPL	240
Qy	181	ASWGGSIPBEERLKAVALTMTLARGIIRPVIGFSIPMSIYACGLIAAKHKMKKSRRPL	240
Db	181	ASWGTAABEELINIAVTPEFVTRGSIFFIIGFIPMSIYACGLIAVKIHRPLANSRRPL	240
Qy	241	RVLITANVASFFICWPPFQVALLGTVMLEKMLFYKRYKTIIDLVNPPSSLAFFVSCINPM	300
Qy	241	RVLITANVASFFICWPPFQVALLGTVMLEKMLFYKRYKTIIDLVNPPSSLAFFVSCINPM	300
Db	241	RVLITANVASFFICWPPFQVALLGTVMLEKESLFSGRYKTIIDLVNWHPTSLAYFVSCINPM	300
Qy	301	LVYFVGQDRERLIHSILPSTLERALSBSGAPINDPNAASPPAETELQAM	351
Qy	301	LVYFVGQDRERLIHSILPSTLERALSBSGAPINDPNAASPPAETELQAM	351
Db	301	LVAFVQDQDHERLIIHSILPSTLERALSBSGQSTDGISALPANNIDIKAI	351

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RESULT 11
US-10-505-486-118
; Sequence 118, Application US/10505486
; Publication No. US20050118639A1
;
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILE REFERENCE: P03-0006PCT
; CURRENT APPLICATION NUMBER: US/10/505,486
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 118
; LENGTH: 591
; TYPE: PRT
;
; ORGANISM: Human
;
; US-10-505-486-118

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Query March	73.0%	Score 1327	DB 5	Length 591
Similarity	72.2%	Pred. No. 9.3e-106		
Best Local				
Matches 255	Conservative 38	Mismatches 58	Indels 2	Gaps 1

Accession	Sequence	Position
Db	1 MEINFSLPNMTTEEVLPPBPAGHTVIMTISLVHGVTLPFGVLGNGVLVIMWAGFNMTRIVN	60
Qy	61 TICYNLALADPSFTATLPELLIVSMAMGEKMPFGNFKLTHIVVDINLFGSVFLIGFIA	120
Db	61 TICYNLALADPSFSALIPFRMVSVAMGEKMPFGSFKLTHVMIDINLFSVYLITIIA	120
Qy	121 LDRICICVLHPVAAQNHRTVSLAMKVIYLPWILATVLTLPVFELTTLVTPNSDFTCFNF	180
Db	121 LDRICICVLHPVAAQNHRTVSLAMKRVMTGMLFTYLLIPNPLFTWTTISTNGDIYCINF	180
Qy	181 ASWGTEPEERLKVAILTMLTARGILIREVIGFSLPMSIVAICYGLIAAKIHKMGKIMSSBPL	240

Db 181 AAMGPTAVERLNAVPTMAKVFLLHFIIGFSVPMISITVCYGLIAAKHHNMKSRPL 240

Qy 241 RVLTVAVASFFICMPPFOLVALLGTWMLKENTLFGKTKIIDLVNPFSSLAFFRSCINPM 300

Db 241 RFAAVVAVASFFICMPPPYELIGILMAVMKEMLNGTKIILVLINPSSLAFFNSCINPI 300

Qy 301 LVVPAAGDPRERLIHSLPTSLERALSE--DSAPNDPAANASAPPAETELQAM 351

Db 301 LVVPAAGDPRERLIHSLPTSLERALTEVPSDAQNSNDITTSAPPEETELQAM 353

```

RESULT 12
US-10-225-567A-633
/ Sequence 633, Application US/10225567A
/ Publication No. US20030113798A1
/ GENERAL INFORMATION:
/ APPLICANT: LifeSpan Biosciences
/ APPLICANT: Brown, Joseph P.
/ APPLICANT: Burner, Glenna C.
/ APPLICANT: Roush, Christine L.
/ TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
/ FILE REFERENCE: 1920-4-4
/ CURRENT APPLICATION NUMBER: US/10/225,567A
/ CURRENT FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 60/257,144
/ PRIOR FILING DATE: 2000-12-19
/ NUMBER OF SEQ ID NOS: 2292
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 633
/ LENGTH: 353
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ US-10-225-567A-633

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Query Match	72.5%;	Score 1318;	DB 4;	Length 353;
Best Local Similarity	71.7%;	Pred. No. 3.1e-105;		
Matches 253;	Conservative 39;	Mismatches 59;	Indels 2;	Gaps 1;

Qy	1	MEINNSTPLNKEEBSYESAGTVLRIPLVLVLTGVLGGLVYIWAAGFEMTEVTY	60
Db	1	MEINNSIPLNKEEBSLPEPAGHTVLMFTSLVHGVTYFGVGLGVYIWAAGFEMRTTVN	60
Qy	61	TI CYNTALMADSPFATYLPPLIVSWMAGEKKMPFCMLKIHIWVDNLNFGSVFLIGFIA	120
Db	61	TI CYNTALMADSPFAIIPFRMWSYAKREKKPFPASFLCKLVHWMIDNLNFSVYLIIIA	120
Qy	121	LDRCI CVLHPWAQNHRTVSLAMKVI VGPWILAVLTVLPVFLFTTVTIENGDTYCTFNF	180
Db	121	LDRCI CVLHPWAQNHRMTSLAKRMVGMVFTVLVLPNFIEMTTISTNGDTYCIENF	180
Qy	181	ASMGGTPEERLKVAITMLTANGIIRFVITGSELPMSIYALCYGLIAAKIHKMKMSRPL	240
Db	181	AEWGDTAVERLNVVFTMAKVFLLHFIIIGTFVPMISITVCYGLIAAKIHRHMKMSRPL	240
Qy	241	RVLTVAVASFPICWPPQVALLGVTMLKEMLFGTKYKIIDLVNPTSSSLAFNSCINPM	3000
Db	241	RVAFAVAVASFPICWPPYELIGILMAVMKEMLNGKXKIIIVLNPTSSSLAFNSCINPI	3000
Qy	301	LVPVPGODRERLIHSLPTSLERLASE--DSAPINDPAANSAPAEETELQAM	351
Db	301	LVPVGRNRNQEELIRSLPTSLERALTVEPDSAQTSNHTTSSASPEETELQAM	353

RESULT 13  
US-10-116-275-218  
Sequence 218, Application US/10116275  
Publication No. US20030211476A1  
GENERAL INFORMATION:  
APPLICANT: Elian Pharmaceutical Technology  
APPLICANT: O'Mahony, Daniel J.  
APPLICANT: Brayden, David  
APPLICANT: Byrne, Daragh

```

; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Feyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Feyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-218

Query Match
Best Local Similarity 71.7%; Pred. No. 3,1e-105;
Matches 253; Conservative 39; Mismatches 59; Indels 2; Gaps 1;

72.5%; Score 1318; DB 4; Length 353;
;
Qy 1 METNFTPLNLEYEBSYESAGYTVLRILPLVVLGTVFVLGNGLVIVWAGFRMTRTYT 60
Db 1 METNFTPLNLEYEBSYESAGYTVLRILPLVVLGTVFVLGNGLVIVWAGFRMTRTYN 60
Qy 61 TICYLNALADSFATLPLPLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVPLIGFTA 120
Db 61 TICYLNALADSFATLPLPLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVPLIGFTA 120
Qy 121 LDRICVLHPVAQNHRVSLAMKVIQVPMIALVLTLPVLEPLTFTVTIPNGDYCTENF 180
Db 121 LDRICVLHPVAQNHRVSLAMKVIQVPMIALVLTLPVLEPLTFTVTIPNGDYCTENF 180
Qy 181 ASWGGPBEERLKVATMLTARGIIRFVIGFSLPMGSIIVACGLIAKHKKGMKSSRPL 240
Db 181 ASWGGPBEERLKVATMLTARGIIRFVIGFSLPMGSIIVACGLIAKHKKGMKSSRPL 240
Qy 241 RVLTAVVASFPCWPFQVALLGTVMLEKMLFYKXKIIDILVNPTSLAFNSCLNPM 300
Db 241 RVLTAVVASFPCWPFQVALLGTVMLEKMLFYKXKIIDILVNPTSLAFNSCLNPM 300
Qy 301 LVYFVGDFRERLHSLPISLERALSE--DSAPNTDPAANSASPATTELQAM 351
Db 301 LVYFVGDFRERLHSLPISLERALSE--DSAPNTDPAANSASPATTELQAM 351
Qy 301 LVYFVGDFRERLHSLPISLERALSE--DSAPNTDPAANSASPATTELQAM 351
Db 301 LVYFVGDFRERLHSLPISLERALSE--DSAPNTDPAANSASPATTELQAM 351

RESULT 14
US-10-789-241-12
; Sequence 12, Application US/10789241
; Publication No. US20040180332A1
; GENERAL INFORMATION:
; APPLICANT: Powell, Douglas M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING 9145, 1725, 311, 837,
; TITLE OF INVENTION: 58305, 156, 14175, 50352, 32678, 5560, 7240, 8865, 12396,
; TITLE OF INVENTION: 12397, 13644, 19938, 2077, 1735, 1786, 10220, 17822, 33945,
; TITLE OF INVENTION: 43748, 47161, 81982 OR 46777
; FILE REFERENCE: MPT03-041P1RNMNMIM
; CURRENT APPLICATION NUMBER: US/10/789,241
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/454,202
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/456,326
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/465,240
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 60/475,233
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 60/478,952
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/487,836
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: US 60/500,111
; PRIOR FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 53

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-241-12

Query Match
Best Local Similarity 72.5%; Score 1318; DB 4; Length 353;
Matches 253; Conservative 39; Mismatches 59; Indels 2; Gaps 1;

72.5%; Score 1318; DB 5; Length 353;
;
Qy 1 METNFTPLNLEYEBSYESAGYTVLRILPLVVLGTVFVLGNGLVIVWAGFRMTRTYT 60
Db 1 METNFTPLNLEYEBSYESAGYTVLRILPLVVLGTVFVLGNGLVIVWAGFRMTRTYN 60
Qy 61 TICYLNALADSFATLPLPLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVPLIGFTA 120
Db 61 TICYLNALADSFATLPLPLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVPLIGFTA 120
Qy 121 LDRICVLHPVAQNHRVSLAMKVIQVPMIALVLTLPVLEPLTFTVTIPNGDYCTENF 180
Db 121 LDRICVLHPVAQNHRVSLAMKVIQVPMIALVLTLPVLEPLTFTVTIPNGDYCTENF 180
Qy 181 ASWGGPBEERLKVATMLTARGIIRFVIGFSLPMGSIIVACGLIAKHKKGMKSSRPL 240
Db 181 ASWGGPBEERLKVATMLTARGIIRFVIGFSLPMGSIIVACGLIAKHKKGMKSSRPL 240
Qy 241 RVLTAVVASFPCWPFQVALLGTVMLEKMLFYKXKIIDILVNPTSLAFNSCLNPM 300
Db 241 RVLTAVVASFPCWPFQVALLGTVMLEKMLFYKXKIIDILVNPTSLAFNSCLNPM 300
Qy 301 LVYFVGDFRERLHSLPISLERALSE--DSAPNTDPAANSASPATTELQAM 351
Db 301 LVYFVGDFRERLHSLPISLERALSE--DSAPNTDPAANSASPATTELQAM 351

RESULT 15
US-10-517-956-14
; Sequence 14, Application US/10517956
; Publication No. US2005023326A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Novel Screening Method
; FILE REFERENCE: 3067W00P
; CURRENT APPLICATION NUMBER: US/10/517,956
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: JP 2002-173798
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: JP 2002-205470
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 14
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Human
US-10-517-956-14

Query Match
Best Local Similarity 71.7%; Pred. No. 3,1e-105;
Matches 253; Conservative 39; Mismatches 59; Indels 2; Gaps 1;

72.5%; Score 1318; DB 5; Length 353;
;
Qy 1 METNFTPLNLEYEBSYESAGYTVLRILPLVVLGTVFVLGNGLVIVWAGFRMTRTYT 60
Db 1 METNFTPLNLEYEBSYESAGYTVLRILPLVVLGTVFVLGNGLVIVWAGFRMTRTYN 60
Qy 61 TICYLNALADSFATLPLPLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVPLIGFTA 120
Db 61 TICYLNALADSFATLPLPLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVPLIGFTA 120
Qy 121 LDRICVLHPVAQNHRVSLAMKVIQVPMIALVLTLPVLEPLTFTVTIPNGDYCTENF 180
Db 121 LDRICVLHPVAQNHRVSLAMKVIQVPMIALVLTLPVLEPLTFTVTIPNGDYCTENF 180
Qy 181 ASWGGPBEERLKVATMLTARGIIRFVIGFSLPMGSIIVACGLIAKHKKGMKSSRPL 240
Db 181 ASWGGPBEERLKVATMLTARGIIRFVIGFSLPMGSIIVACGLIAKHKKGMKSSRPL 240
Qy 241 RVLTAVVASFPCWPFQVALLGTVMLEKMLFYKXKIIDILVNPTSLAFNSCLNPM 300
Db 241 RVLTAVVASFPCWPFQVALLGTVMLEKMLFYKXKIIDILVNPTSLAFNSCLNPM 300
Qy 301 LVYFVGDFRERLHSLPISLERALSE--DSAPNTDPAANSASPATTELQAM 351
Db 301 LVYFVGDFRERLHSLPISLERALSE--DSAPNTDPAANSASPATTELQAM 351

```

QY 181 ASWGGTPEERLKVAITMLTARGIIRFVIGPSLEMSIVAICYGLIAAKIHKKMIKSSRPL 240  
| | | | | : | | | | : | | | | : | | | |  
Db 181 AFMGDTAVERLNVFITWAKVFLIHFIIGFTVPMIITVCYGLIAAKIHRHMIKSSRPL 240  
| | | | | : | | | | : | | | | : | | | |  
QY 241 RVLTAVASPFICMPEPQVALLGTVMLKEMLFYGYKIIDIVNPTSSLAFFNSCLNPM 300  
| | | | | : | | | | : | | | | : | | | |  
Db 241 RVFAAVVASPFICMPEYELIGILMAVWLKEMLNGKYKIIVLINPTSSLAFFNSCLNPI 300  
| | | | | : | | | | : | | | | : | | | |  
QY 301 LYYFVGQDFRERLIHSLPTSLERALSE--DSAPTNDTAANSASPPAETELQAM 351  
| | | | | : | | | | : | | | | : | | | |  
Db 301 LYYFMGRNFQERLIRSLPTSLERALTEVPDSAQTSNHTTSASPRETELQAM 353  
| | | | | : | | | | : | | | | : | | | |

Search completed: March 28, 2006, 13:26:03  
Job time : 216.344 secs

1:

1.

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Db 301 LVFVGGDFRRLIHSLSPTSLERLSEDSAPTNDTANASPPAETELQAM 351

RESULT 2  
US-11-218-281-24

Sequence 24, Application US/11218281  
Publication No. US20060024758A1  
GENERAL INFORMATION:  
APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.  
APPLICANT: Serhan, Charles N.  
APPLICANT: Ariza, Makoto  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY  
FILE REFERENCE: MP-14448.05  
CURRENT APPLICATION NUMBER: US/11/218,281  
CURRENT FILING DATE: 2005-09-01  
PRIOR APPLICATION NUMBER: 60/452,244  
PRIOR FILING DATE: 2003-03-05  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 24  
LENGTH: 351  
TYPE: PRT  
ORGANISM: HOMO SAPIENS  
US-11-218-281-24

Query Match 100.0%; Score 1817; DB 7; Length 351;  
Best Local Similarity 100.0%; Pred. No. 2,1e-136;  
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNSTPLNNEYEVSYSAGYVLRILPLVLTGVTPLGNGLVIVVAGFRMTRTYT 60  
DB 1 METNSTPLNNEYEVSYSAGYVLRILPLVLTGVTPLGNGLVIVVAGFRMTRTYT 60  
QY 61 TICYLNLALADSFATLPLPLIVSMAMGKMPGFWFLCKLHIIVVDINLFGSVFLIGFTA 120  
DB 61 TICYLNLALADSFATLPLPLIVSMAMGKMPGFWFLCKLHIIVVDINLFGSVFLIGFTA 120  
QY 121 LDRICICVLHPVMAQNHRVTSLSAMKVIIVGFWILAVLTPVFLPTVTTPNGDTCYCFNF 180  
DB 121 LDRICICVLHPVMAQNHRVTSLSAMKVIIVGFWILAVLTPVFLPTVTTPNGDTCYCFNF 180  
QY 181 ASWGTPEERLKVATIMLTARGIIRFVIGFSLPMSIVACYGLIAKIHKKGMKISSRPL 240  
DB 181 ASWGTPEERLKVATIMLTARGIIRFVIGFSLPMSIVACYGLIAKIHKKGMKISSRPL 240  
QY 241 RVLTAVASFFICWPPQVALIGTVMLEKMLFYGKYKIIDLVNPTSSLAFFNSCLNPM 300  
DB 241 RVLTAVASFFICWPPQVALIGTVMLEKMLFYGKYKIIDLVNPTSSLAFFNSCLNPM 300  
QY 301 LVFVGGDFRRLIHSLSPTSLERLSEDSAPTNDTANASPPAETELQAM 351  
DB 301 LVFVGGDFRRLIHSLSPTSLERLSEDSAPTNDTANASPPAETELQAM 351

RESULT 3  
US-11-218-281-25

Sequence 25, Application US/11218281  
Publication No. US20060024758A1  
GENERAL INFORMATION:  
APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.  
APPLICANT: Serhan, Charles N.  
APPLICANT: Ariza, Makoto  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY  
FILE REFERENCE: MP-14448.05  
CURRENT APPLICATION NUMBER: US/11/218,281  
CURRENT FILING DATE: 2005-09-01  
PRIOR APPLICATION NUMBER: 60/452,244  
PRIOR FILING DATE: 2003-03-05  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn version 3.2

SEQ ID NO 25  
LENGTH: 353  
TYPE: PRT  
ORGANISM: HOMO SAPIENS  
US-11-218-281-25

Query Match 73.0%; Score 1327; DB 7; Length 353;  
Best Local Similarity 72.2%; Pred. No. 1e-97;  
Matches 255; Conservative 38; Mismatches 58; Indels 2; Gaps 1;

QY 1 METNSTPLNNEYEVSYSAGYVLRILPLVLTGVTPLGNGLVIVVAGFRMTRTYT 60  
DB 1 METNSTPLNNEYEVSYSAGYVLRILPLVLTGVTPLGNGLVIVVAGFRMTRTYT 60  
QY 61 TICYLNLALADSFATLPLPLIVSMAMGKMPGFWFLCKLHIIVVDINLFGSVFLIGFTA 120  
DB 61 TICYLNLALADSFATLPLPLIVSMAMGKMPGFWFLCKLHIIVVDINLFGSVFLIGFTA 120  
QY 121 LDRICICVLHPVMAQNHRVTSLSAMKVIIVGFWILAVLTPVFLPTVTTPNGDTCYCFNF 180  
DB 121 LDRICICVLHPVMAQNHRVTSLSAMKVIIVGFWILAVLTPVFLPTVTTPNGDTCYCFNF 180  
QY 181 ASWGTPEERLKVATIMLTARGIIRFVIGFSLPMSIVACYGLIAKIHKKGMKISSRPL 240  
DB 181 ASWGTPEERLKVATIMLTARGIIRFVIGFSLPMSIVACYGLIAKIHKKGMKISSRPL 240  
QY 241 RVLTAVASFFICWPPQVALIGTVMLEKMLFYGKYKIIDLVNPTSSLAFFNSCLNPM 300  
DB 241 RVLTAVASFFICWPPQVALIGTVMLEKMLFYGKYKIIDLVNPTSSLAFFNSCLNPM 300  
QY 301 LVFVGGDFRRLIHSLSPTSLERLSEDSAPTNDTANASPPAETELQAM 351  
DB 301 LVFVGGDFRRLIHSLSPTSLERLSEDSAPTNDTANASPPAETELQAM 351

RESULT 4  
US-10-508-765-2

Sequence 2, Application US/10508765  
Publication No. US2006005757A1  
GENERAL INFORMATION:  
APPLICANT: Golz, Stefan  
APPLICANT: Bruggemeier, Ulf  
TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with Homo  
FILE REFERENCE: Le A 35 838  
CURRENT APPLICATION NUMBER: US/10/508,765  
CURRENT FILING DATE: 2004-09-22  
PRIOR APPLICATION NUMBER: PCT/EP03/02414  
PRIOR FILING DATE: 2003-03-10  
PRIOR APPLICATION NUMBER: EP 02006595.9  
PRIOR FILING DATE: 2002-03-22  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 2  
LENGTH: 353  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-508-765-2

Query Match 72.5%; Score 1318; DB 6; Length 353;  
Best Local Similarity 71.7%; Pred. No. 5.2e-97;  
Matches 253; Conservative 39; Mismatches 59; Indels 2; Gaps 1;

QY 1 METNSTPLNNEYEVSYSAGYVLRILPLVLTGVTPLGNGLVIVVAGFRMTRTYT 60  
DB 1 METNSTPLNNEYEVSYSAGYVLRILPLVLTGVTPLGNGLVIVVAGFRMTRTYT 60  
QY 61 TICYLNLALADSFATLPLPLIVSMAMGKMPGFWFLCKLHIIVVDINLFGSVFLIGFTA 120  
DB 61 TICYLNLALADSFATLPLPLIVSMAMGKMPGFWFLCKLHIIVVDINLFGSVFLIGFTA 120  
QY 121 LDRICICVLHPVMAQNHRVTSLSAMKVIIVGFWILAVLTPVFLPTVTTPNGDTCYCFNF 180  
DB 121 LDRICICVLHPVMAQNHRVTSLSAMKVIIVGFWILAVLTPVFLPTVTTPNGDTCYCFNF 180

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Db      121 LDRICVLHPMAQONHRTMSLAKRVMGMIFITVLPLPFIWTTISTNGTYCENF 160
Qy      181 ASNGTPEERLKAITMTLTARGIIRFVIGSLPMSIYACGLIAKHKKMKSRPL 240
Db      181 AFNGDPAVERLNVITMAKFLIHPITIGTVPMSITTCYCGIAKHKKMKSRPL 240
Qy      241 RVLTAVASFFICMPFPQVALVGLTWLKMELFYGKXKIIDIVNPTSSLAFFNSCLNPM 300
Db      241 RVPAAVASFFICMPFELIGILMAVWLKEMLNGKXKILVILNPTSSLAFFNSCLNPM 300
Qy      301 LYFVGODFERRLIHSIPTSLERALS--DSAPNDTAAASAPPAETELQAM 351
Db      301 LYFVGMRNFOERLIRSLIPTSLERALTVPDSAQTSNHTTSSASPEETELQAM 353

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RESULT 5
US-11-218-281-23
; Sequence 23, Application US/11218281
; Publication No. US20060024758A1
; GENERAL INFORMATION:
; APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
; APPLICANT: Sethan, Charles N.
; APPLICANT: Arita, Makoto
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
; TITLE OF INVENTION: RECEPTORS FOR EICOSAPENTAENOIC ACID ANALOGS
; FILE REFERENCE: MP-14448-05
; CURRENT APPLICATION NUMBER: US/11/218, 281
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: 60/452,244
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 23
; LENGTH: 350
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-11-218-281-23

```

```

Query Match      68.4%; Score 1243.5; DB 7; Length 350;
Best Local Similarity 68.6%; Pred. No. 3,9e-91;
Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;

Qy      1 METNFSPTLNEVEEVSYSAGYTVLRILPLVGLVGTFLVGLNGVIVWAGFRMTRTYT 60
Db      1 METNSSLPTNISGTPVSVAGYLFLLDITTYLVRAVTVVGLVGLNGVIVWAGFRMTHVT 60
Qy      61 TICVNLALADFSFTATLPLIVSMANGKMPFGMFLCKLIHIVVDINLFGSVFLIGFIA 120
Db      61 TISTNLAVADFCFTSTLPLFPMVKAMGHPFCMFLCKFLFTVIDINLFGSVFLIALIA 120
Qy      121 LDRICVLHPMAQONHRTMSLAKRVMGMIFITVLPLPFIWTTISTNGTYCENF 180
Db      121 LDRICVLHPMAQONHRTMSLAKRVMGMIFITVLPLPFIWTTISTNGTYCENF 180
Qy      121 LDRICVLHPMAQONHRTMSLAKRVMGMIFITVLPLPFIWTTISTNGTYCENF 180
Db      121 LDRICVLHPMAQONHRTMSLAKRVMGMIFITVLPLPFIWTTISTNGTYCENF 180
Qy      181 ASNGTPEERLKAITMTLTARGIIRFVIGSLPMSIYACGLIAKHKKMKSRPL 240
Db      181 ASNGTPEERLKAITMTLTARGIIRFVIGSLPMSIYACGLIAKHKKMKSRPL 240
Qy      181 SPWINDKERLNVAVAMLVIRGIIIRFIIGSAPMSIYAVSGILATIKHKKMKSRPL 240
Db      181 SPWINDKERLNVAVAMLVIRGIIIRFIIGSAPMSIYAVSGILATIKHKKMKSRPL 240
Qy      241 RVLTAVASFFICMPFPQVALVGLTWLKMELFYGKXKIIDIVNPTSSLAFFNSCLNPM 300
Db      241 RVLTAVASFFICMPFPQVALVGLTWLKMELFYGKXKIIDIVNPTSSLAFFNSCLNPM 300
Qy      241 RVLTAVASFFICMPFPQVALVGLTWLKMELFYGKXKIIDIVNPTSSLAFFNSCLNPM 300
Db      241 RVLTAVASFFICMPFPQVALVGLTWLKMELFYGKXKIIDIVNPTSSLAFFNSCLNPM 300
Qy      301 LYFVGODFERRLIHSIPTSLERALS--DSAPNDTAAASAPPAETELQAM 350
Db      301 LYFVGODFERRLIHSIPTSLERALS--DSAPNDTAAASAPPAETELQAM 350

```

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RESULT 6
US-11-218-281-27
; Sequence 27, Application US/11218281
; Publication No. US20060024758A1
; GENERAL INFORMATION:

```

```

; APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
; APPLICANT: Sethan, Charles N.
; APPLICANT: Arita, Makoto
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
; TITLE OF INVENTION: RECEPTORS FOR EICOSAPENTAENOIC ACID ANALOGS
; FILE REFERENCE: MP-14448-05
; CURRENT APPLICATION NUMBER: US/11/218, 281
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: 60/452,244
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 27
; LENGTH: 356
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-11-218-281-27

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Query Match      30.5%; Score 553.5; DB 7; Length 356;
Best Local Similarity 41.0%; Pred. No. 1.2e-36;
Matches 126; Conservative 59; Mismatches 113; Indels 9; Gaps 4;

Qy      25 LRLPLVGLVGTFLVGLNGVIVWAGFRMTRTYTTCVNLALADFSFTATLP--PL 81
Db      42 LRLPLVGLVGTFLVGLNGVIVWAGFRMTRTYTTCVNLALADFSFTATLP--PL 101
Qy      82 IVSMANGKMPFGMFLCKLIHIVVDINLFGSVFLIGFIALDRICVLHPMAQONHRTVSL 141
Db      102 IVS----RQMLGEMAKXKIYTFVFLSYFASNLVLFISVDCISVLYPVMLNHRVTOR 157
Qy      142 AMKVIVGPMILAVLTLPVFLFTTYTNGDTYCTCFNPSMGCTPEERLKAITMTLTAR 201
Db      158 ASWLAGVWLMLAALCSAHLKFTTRKW--NGCHCYLAIRNSDNETQIIVGVEGHIIG 216
Qy      202 GTRFVIGSLPMSIYACGLIAKHKKMKSRPLRVLTAVASFFICMPFQVALV 261
Db      217 TIGFPLGFGPLATIGTCHLIRAKLRLBGMVHARKPRLLVLSAFPIFSPRNV- 275
Qy      262 LIGTWMKEMLFYGKXKIIDIVNPTSSLAFFNSCLNPMLYFVGODFERRLIHSPTSL 321
Db      276 LVLHMRVWLKXIYPRMLILIQASFALGCVNSSLNPLFYVVGGRDFOKRFQSLTSL 335
Qy      322 ERALSD 328
Db      336 ARAFGEE 342

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RESULT 7
US-11-134-811-4
; Sequence 4, Application US/11134811
; Publication No. US20060024750A1
; GENERAL INFORMATION:
; APPLICANT: Wiltamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandebogaerde, Ann
; APPLICANT: Decheux, Michel
; APPLICANT: Parentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerin
; FILE REFERENCE: 9409/2043
; CURRENT APPLICATION NUMBER: US/11/134, 811
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: PCT/EP02/07647
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1

```

SEQ ID NO 4  
LENGTH: 371  
TYPE: PRN  
ORGANISM: Mus musculus  
US-11-134-811-4

Query Match 29.6%; Score 538.5; DB 7; Length 371;  
Best Local Similarity 35.2%; Pred. No. 1.9e-35;  
Matches 120; Conservative 70; Mismatches 124; Indels 27; Gaps 8;

10 NEYES-----VSYESAGYTVLRILP---LVVLGTVFVLGNGLVIVWAGFMRTRVT 61  
DB DEYSDEGFGYVDLEESAPWEAKAVPFLVIVYSLVCFGLGNGLVIVATFPMKKTAVNT 73  
QY 62 ICYNLALADFSFTATLPFLIVSMANGKMPFGMFLCKLIHIVDINLFGSVFLIGFIAL 121  
DB 74 VWFVNLAADVDFLNFILPMTITAAADYHNVFGKAMCKISNFLSHNMTYSVLLTVISF 133  
QY 122 DRCICVLHPVMAONHRTVSLAMKVIYGPWILALVLTLPVFLFTTYTTPNGDTYCTFNPA 181  
DB 134 DRCISVLLPWSQNHRSIRLAIVMTCSAVWVLAFLSPSLVFRDTANI-HGKITCFNNFS 192  
QY 182 SWGCTPEERLKAIVMTLARG-----IIRFVIGSLPMSIVATCYGLIAKHKKGM 233  
DB 193 L--AAPBESSPHASQVSTGSRHVAVTYRFLCGFLIPVITACVLTTFVKLQNRRL 250  
QY 234 IKSRRLRLVLTAVASFFICWPFQVALLGTVMLEKMLFYGKYKIIDILVNP-TSSLA 292  
DB 251 AKKKKPKIITITITFLFCMCPYH-----TLVLELHHTHRAVPSVSGLPLATAVAI 304  
QY 293 FNSCLNPMLYVFVGDFFERLHSLPTSLERALSSEDAPTN 333  
DB 305 ANSCMNPILYVFMGHDFFRKFV-ALFSRLANLALSDTGSS 344

RESULT 8  
US-11-218-281-2  
Sequence 2, Application US/11218281  
Publication No. US20060024758A1  
GENERAL INFORMATION:  
APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.  
APPLICANT: Serhan, Charles N.  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY  
FILE REFERENCE: MP-14448.05  
CURRENT APPLICATION NUMBER: US/11/218,281  
PRIOR FILING DATE: 2005-09-01  
PRIOR FILING DATE: 2003-03-05  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2  
LENGTH: 371  
TYPE: PRN  
ORGANISM: MOUSE  
US-11-218-281-2

Query Match 29.6%; Score 538.5; DB 7; Length 371;  
Best Local Similarity 35.2%; Pred. No. 1.9e-35;  
Matches 120; Conservative 70; Mismatches 124; Indels 27; Gaps 8;

10 NEYES-----VSYESAGYTVLRILP---LVVLGTVFVLGNGLVIVWAGFMRTRVT 61  
DB DEYSDEGFGYVDLEESAPWEAKAVPFLVIVYSLVCFGLGNGLVIVATFPMKKTAVNT 73  
QY 62 ICYNLALADFSFTATLPFLIVSMANGKMPFGMFLCKLIHIVDINLFGSVFLIGFIAL 121  
DB 74 VWFVNLAADVDFLNFILPMTITAAADYHNVFGKAMCKISNFLSHNMTYSVLLTVISF 133  
QY 122 DRCICVLHPVMAONHRTVSLAMKVIYGPWILALVLTLPVFLFTTYTTPNGDTYCTFNPA 181  
DB 134 DRCISVLLPWSQNHRSIRLAIVMTCSAVWVLAFLSPSLVFRDTANI-HGKITCFNNFS 192

QY 182 SWGCTPEERLKAIVMTLARG-----IIRFVIGSLPMSIVATCYGLIAKHKKGM 233  
DB 193 L--AAPBESSPHASQVSTGSRHVAVTYRFLCGFLIPVITACVLTTFVKLQNRRL 250  
QY 234 IKSRRLRLVLTAVASFFICWPFQVALLGTVMLEKMLFYGKYKIIDILVNP-TSSLA 292  
DB 251 AKKKKPKIITITITFLFCMCPYH-----TLVLELHHTHRAVPSVSGLPLATAVAI 304  
QY 293 FNSCLNPMLYVFVGDFFERLHSLPTSLERALSSEDAPTN 333  
DB 305 ANSCMNPILYVFMGHDFFRKFV-ALFSRLANLALSDTGSS 344

RESULT 9  
US-11-218-281-33  
Sequence 33, Application US/11218281  
Publication No. US20060024758A1  
GENERAL INFORMATION:  
APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.  
APPLICANT: Serhan, Charles N.  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY  
FILE REFERENCE: MP-14448.05  
CURRENT APPLICATION NUMBER: US/11/218,281  
PRIOR FILING DATE: 2005-09-01  
PRIOR FILING DATE: 2003-03-05  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 33  
LENGTH: 371  
TYPE: PRN  
ORGANISM: MOUSE  
US-11-218-281-33

Query Match 29.6%; Score 538.5; DB 7; Length 371;  
Best Local Similarity 35.2%; Pred. No. 1.9e-35;  
Matches 120; Conservative 70; Mismatches 124; Indels 27; Gaps 8;

10 NEYES-----VSYESAGYTVLRILP---LVVLGTVFVLGNGLVIVWAGFMRTRVT 61  
DB DEYSDEGFGYVDLEESAPWEAKAVPFLVIVYSLVCFGLGNGLVIVATFPMKKTAVNT 73  
QY 62 ICYNLALADFSFTATLPFLIVSMANGKMPFGMFLCKLIHIVDINLFGSVFLIGFIAL 121  
DB 74 VWFVNLAADVDFLNFILPMTITAAADYHNVFGKAMCKISNFLSHNMTYSVLLTVISF 133  
QY 122 DRCICVLHPVMAONHRTVSLAMKVIYGPWILALVLTLPVFLFTTYTTPNGDTYCTFNPA 181  
DB 134 DRCISVLLPWSQNHRSIRLAIVMTCSAVWVLAFLSPSLVFRDTANI-HGKITCFNNFS 192  
QY 182 SWGCTPEERLKAIVMTLARG-----IIRFVIGSLPMSIVATCYGLIAKHKKGM 233  
DB 193 L--AAPBESSPHASQVSTGSRHVAVTYRFLCGFLIPVITACVLTTFVKLQNRRL 250  
QY 234 IKSRRLRLVLTAVASFFICWPFQVALLGTVMLEKMLFYGKYKIIDILVNP-TSSLA 292  
DB 251 AKKKKPKIITITITFLFCMCPYH-----TLVLELHHTHRAVPSVSGLPLATAVAI 304  
QY 293 FNSCLNPMLYVFVGDFFERLHSLPTSLERALSSEDAPTN 333  
DB 305 ANSCMNPILYVFMGHDFFRKFV-ALFSRLANLALSDTGSS 344

RESULT 10  
US-11-134-811-2  
Sequence 2, Application US/11134811  
Publication No. US20060024750A1  
GENERAL INFORMATION:  
APPLICANT: Wiltamier, Valerie  
APPLICANT: Communi, David

```

; APPLICANT: Vandenberg, Ann
; APPLICANT: Decheux, Michel
; APPLICANT: Parentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerin
; FILE REFERENCE: 9409/2003
; CURRENT APPLICATION NUMBER: US/11/134,811
; PRIOR FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: PCT/EP02/07647
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-134-811-2

Query Match
Best Local Similarity 29.4%; Score 534.5; DB 7; Length 371;
Matches 122; Conservative 65; Mismatches 130; Indels 19; Gaps 7;

QY 24 VRIILPLVVLGVTVFVGLVGLVGLVIVVAGFRMTRTVTTCYLNALADSFATLPLFLIV 83
DB 36 VRIILPLVVLGVTVFVGLVGLVGLVIVVAGFRMTRTVTTCYLNALADSFATLPLFLIH 95
QY 84 SNAMGEKWPFGWFLCKLHIIVVDINLFGSVFLIGFIALDRICIVLHPVAAQNHRTYSLAM 143
DB 96 YAMADYHWVFGTAMCKISNFIILHNMFTSVFLITLTISSDRICISVLLPWSQNHRSVRLAY 155
QY 144 KVIYGPWILALVTLPLVFLFTVTTPNGDYCTFNF-----ASWGTPEBRLLKVAIT 196
DB 156 MACMTWVLAFLPSSPSLVFRDPTANL-HGKISCNNFSLSTPGSSW-PTHSQMDPVGIS 213
QY 197 MLTARGIIRFVIGFSLPMSIVAICYGLIAKIKKGMKISSRPLRLVLAIVASFFICWPP 256
DB 214 RHVVTVTRFLGFLVPLVLTITACVITIVCKLQRNRATKKPKIIVTIIITFLCWCP 273
QY 257 FQVALLGTWVKEMLFYGYKXIIDLIVNPTSSLAFFNSCLNPLVYFGQDFRRLIHS 316
DB 274 YHTLNLLE---LHHTAMPG--SVFSIGLPLATLAIANSQNPDIYVFMGDFKKPKV-A 327
QY 317 LPTSLERALSSED-----SAPTNDTAANSAPPAETEL 348
DB 328 LFSRLVNALSEDTGHSSYPHSRSTTKMSMNERTISM 363

RESULT 11
US-11-218-281-1
; Sequence 1, Application US/11218281
; Publication No. US20060024758A1
; GENERAL INFORMATION:
; APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
; APPLICANT: Artea, Makoto
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
; FILE REFERENCE: MP-14448-05
; CURRENT APPLICATION NUMBER: US/11/218,281
; PRIOR FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: 60/452,244
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 373

```

```

; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-11-218-281-1

Query Match
Best Local Similarity 29.4%; Score 534.5; DB 7; Length 373;
Matches 122; Conservative 65; Mismatches 130; Indels 19; Gaps 7;

QY 24 VRIILPLVVLGVTVFVGLVGLVGLVIVVAGFRMTRTVTTCYLNALADSFATLPLFLIV 83
DB 36 VRIILPLVVLGVTVFVGLVGLVGLVIVVAGFRMTRTVTTCYLNALADSFATLPLFLIH 97
QY 84 SNAMGEKWPFGWFLCKLHIIVVDINLFGSVFLIGFIALDRICIVLHPVAAQNHRTYSLAM 143
DB 98 YAMADYHWVFGTAMCKISNFIILHNMFTSVFLITLTISSDRICISVLLPWSQNHRSVRLAY 157
QY 144 KVIYGPWILALVTLPLVFLFTVTTPNGDYCTFNF-----ASWGTPEBRLLKVAIT 196
DB 158 MACMTWVLAFLPSSPSLVFRDPTANL-HGKISCNNFSLSTPGSSW-PTHSQMDPVGIS 215
QY 197 MLTARGIIRFVIGFSLPMSIVAICYGLIAKIKKGMKISSRPLRLVLAIVASFFICWPP 256
DB 216 RHVVTVTRFLGFLVPLVLTITACVITIVCKLQRNRATKKPKIIVTIIITFLCWCP 275
QY 257 FQVALLGTWVKEMLFYGYKXIIDLIVNPTSSLAFFNSCLNPLVYFGQDFRRLIHS 316
DB 276 YHTLNLLE---LHHTAMPG--SVFSIGLPLATLAIANSQNPDIYVFMGDFKKPKV-A 329
QY 317 LPTSLERALSSED-----SAPTNDTAANSAPPAETEL 348
DB 330 LFSRLVNALSEDTGHSSYPHSRSTTKMSMNERTISM 365

RESULT 12
US-11-218-281-28
; Sequence 28, Application US/11218281
; Publication No. US20060024758A1
; GENERAL INFORMATION:
; APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
; APPLICANT: Artea, Makoto
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
; FILE REFERENCE: MP-14448-05
; CURRENT APPLICATION NUMBER: US/11/218,281
; PRIOR FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: 60/452,244
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-11-218-281-28

Query Match
Best Local Similarity 29.4%; Score 534.5; DB 7; Length 373;
Matches 122; Conservative 65; Mismatches 130; Indels 19; Gaps 7;

QY 24 VRIILPLVVLGVTVFVGLVGLVGLVIVVAGFRMTRTVTTCYLNALADSFATLPLFLIV 83
DB 38 VRIILPLVVLGVTVFVGLVGLVGLVIVVAGFRMTRTVTTCYLNALADSFATLPLFLIH 97
QY 84 SNAMGEKWPFGWFLCKLHIIVVDINLFGSVFLIGFIALDRICIVLHPVAAQNHRTYSLAM 143
DB 98 YAMADYHWVFGTAMCKISNFIILHNMFTSVFLITLTISSDRICISVLLPWSQNHRSVRLAY 157
QY 144 KVIYGPWILALVTLPLVFLFTVTTPNGDYCTFNF-----ASWGTPEBRLLKVAIT 196
DB 158 MACMTWVLAFLPSSPSLVFRDPTANL-HGKISCNNFSLSTPGSSW-PTHSQMDPVGIS 215
QY 197 MLTARGIIRFVIGFSLPMSIVAICYGLIAKIKKGMKISSRPLRLVLAIVASFFICWPP 256

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Db 216 RHVVVTVTFHFGSLVPLVLIITACVLITVICLQGRRLAKTKKPKRIIVITIIITFFELMCSP 275  
 Qy 257 FQIVALLGVTVLKEKMLFYGKTKIIDLIVNPVSSLAFNSCINPMILYVFGODFFERLIHS 316  
 Db 276 YHNLINLE---LHHTAMPG--SVFSIGCLPLAALAIANSNNPILYVFGODFFKPKRY-A 329  
 Qy 317 LPTSLERALSIED----SAPNTDAAANSAPPAETEL 348  
 Db 330 LPSRLVYNALSEDTGHSHSYPSHRSPFKMSNMNERITSM 365

```

RESULT 13
US-10-502-145-1
; Sequence 1, Application US/10502145
; Publication NO. US20050244406A1
; GENERAL INFORMATION:
; APPLICANT: MACKAY, CHARLES REAY
; TITLE OF INVENTION: Anti-C5ar antibodies and uses thereof
; FILE REFERENCE: RICE-032
; CURRENT APPLICATION NUMBER: US/10/502,145
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US$N 60/350,961
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 350
; TYPE: PRN
; ORGANISM: Homo sapiens
; US-10-502-145-1

```

Query Match	28.2%	Score 513;	DB 6;	Length 350;
Best Local Similarity	33.6%	Pred. No. 1.8e-33;		
Matches 122; Conservative	60;	Mismatches 129;	Indels 52;	Gaps 9

```

QY      4 NSTP- LNEYEE-----VSYESAGYVLRLPLVVLGVTVLGVANGVIWAGF   53
       ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      5 NTPTPYGHYDDKDTLDINTPVDKTSNTLRPRDILALIVFAVVELVEGLNALVVWYAF   64

QY      54 RMTRIYVTIT CYANLALADESFTATLLPRLIVSMANGEKMPGEMCLKLIHVVDINFGSV  113
       ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      65 EAKRTINALWFNLNLAADFLSCIALPIFTSIIVGHHHPFGAACSILPILIINNAYASI  124

QY      114 FLIGFALDRCTULHPWAQNHRVRVSLAMKVYGGPWTLALVYLPEFLPLTYTIPND    173
       ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      125 LLALTISARFLLVKRPIMQCNFRAGIAMJACAVMGCLALLTIISPFLRVV-----RE  179

QY      174 TY-----CTPFNASMGGPBEERLVAITALTMLTARGIRFVGFSLPMSIYAICYGLIAAK  227
       ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      180 EYFPFKVCUDVYSH-----DKRRRAY-----AIYRVLVGFMLPILLTTICTYTILNR  228

QY      228 IHKGMIKSRLRYLTVLTVASFFPICWPFPQLVALLGTMVKENLFYGYKKIIDILVNPT   287
       ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      229 TWSRRATRSTKTLKVVAVVVASFFELFWLPYVGTGM-----MSFLBPSPFFLLNKU    281

QY      288 SSL-----AFNSCLAMPILYVFVGODFKERRLIHLSIFTSIERALSDESA-----PTMD  334
       ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      282 DSLCVSFAYINCINCPILIIYVAGOGFCQRKRKSLPSLLRNLTRESVVRESKSPFTRSTD  341

QY      335 TAA  337
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Db      342 TWA  344

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RESULT 14
US-11-169-976-9
; Sequence 9, Application US/11169976
; Publication No. US20060014249A1
; GENERAL INFORMATION:
; APPLICANT: IJ, et al.
; TITLE OF INVENTION: Human G-Protein Coupled Receptor
; FILE REFERENCE: PF159P1C2

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; CURRENT APPLICATION NUMBER: US/11,169,976
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 10/259,521
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: 08/462,314
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US95/01992
; PRIOR FILING DATE: 1995-02-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-169-976-9

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Query Match	28.2%;	Score 513;	DB 7;	Length 350;
Best Local Similarity	33.6%;	Pred. No. 1.8e-33;		
Matches 122; Conservative	60;	Mismatches 129;	Indels 52;	Gaps 9;

[illegible]

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RESULT 15
US-11-218-281-31
/ Sequence 31. Application US/11218281
/ Publication NO. US20060024758A1
/ GENERAL INFORMATION:
/ APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
/ APPLICANT: Serhan, Charles N.
/ APPLICANT: Ariza, Makoto
/ TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
/ TITLE OF INVENTION: RECEPTORS FOR EICOSAPENTAENOIC ACID ANALOGS
/ FILE REFERENCE: MP-14448.05
/ CURRENT APPLICATION NUMBER: US/11/218,281
/ CURRENT FILING DATE: 2005-09-01
/ PRIOR APPLICATION NUMBER: 60/452,244
/ PRIOR FILING DATE: 2003-03-05
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 31
/ LENGTH: 350
/ TYPE: PRF
/ ORGANISM: HOMO SAPIENS
/ US-11-218-281-31

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Query Match 28.2%; Score 513; DB 7; Length 350;

Best Local Similarity 33.6%; Pred. No. 1.8e-33;  
Matches 122; Conservative 60; Mismatches 129; Indels 52; Gaps 9;

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QY      4 NESTP-LINEYB-----VSBSAGYVLRILPLVVGTFPLVGLGGLVYVAGF 53
Db      5 NYTTPOGVGHDDVDLIDLNTLPVDKTSNTLRVDDILALIVPAVPLVGLVGNALVYVNTAF 64

QY      54 RMTRTVTTI CYLNLALADSPFTATLPLPLVSNAMGEKMPFGMFLCKLIHVINDLPGSV 113
Db      65 EAKRTINAIWPLNLAVADFLSCIALPILEPTSIQVHHHPFGGAACSIPLSIILMTYASI 124

QY      114 FLIGFLALDRICIYLRPWAKNHRVLSLAKYIVSPWILAVLPLPVPLFTTYTINGD 173
Db      125 LLLATTSABRFLPLVFPPIWQGNFRGAGLAMIACAVAMELALLLTTPSPFLXRV-----RE 179

QY      174 TY-----CTPNASGWGTPBEERLKAIVTMLTARGIIRFVIGFSPLMSIVCYGLIAAK 227
Db      180 EYPPKVLGVVDYSH-----DKRRERAV-----AIYALVIGFLMPLTLTICTYPIILR 228

QY      228 IHKKGIKSRPLRVLTAIVASPFICWPPFOALAGTVMLEKMLFYGKKYKIDILVNPT 287
Db      229 TWBRATRYSTKLKLVAVVAVASPFIFMLPELYQTGTIM-----MSFLPPSSPTFLINKL 281

QY      288 SGL-----APFNSGLANMLYVPGQDFRRLIHSLETSIERLASDSA-----PTND 334
Db      282 DSIQVSPAYINCINPIIVVAGOGFQGRLRKSLPSLIRNLVLTBSVVRBSKSPTRSTVD 341

QY      335 TAA 337
Db      342 TMA 344

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Search completed: March 28, 2006, 13:26:39

Job time : 30.016 secs

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GenCore version 5.1.7  
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# QOM protein - protein search, using SW model

Run on: March 28, 2006, 13:21:13 ; Search time 14.656 Seconds  
(without alignment)  
684.218 Million cell updates/sec

Title: US-10-517-956-3

Perfect score: 120

Sequence: 1 MAPRGFCLLLTSEIDLPIVKRRA 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_Main:

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*

2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*

3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*

4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*

5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*

6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	24	US-10-306-878-2	Sequence 2, Appli
2	120	100.0	24	US-10-341-434-167	Sequence 167, App
3	120	100.0	24	US-10-341-434-200	Sequence 200, App
4	120	100.0	24	US-10-716-432-1	Sequence 1, Appli
5	120	100.0	24	US-10-852-705A-2	Sequence 2, Appli
6	120	100.0	24	US-10-517-956-3	Sequence 3, Appli
7	120	100.0	24	US-10-514-653-1	Sequence 1, Appli
8	120	100.0	24	US-10-514-653-4	Sequence 4, Appli
9	120	100.0	24	US-10-514-653-5	Sequence 5, Appli
10	120	100.0	24	US-10-514-653-6	Sequence 6, Appli
11	120	100.0	24	US-10-514-653-7	Sequence 7, Appli
12	120	100.0	24	US-10-514-653-8	Sequence 8, Appli
13	120	100.0	24	US-10-514-653-9	Sequence 9, Appli
14	120	100.0	24	US-10-514-653-27	Sequence 27, Appli
15	120	100.0	24	US-10-514-653-17	Sequence 17, Appli
16	117	97.5	24	US-10-514-653-12	Sequence 12, Appli
17	117	97.5	24	US-10-514-653-15	Sequence 15, Appli
18	116	96.7	24	US-10-517-956-4	Sequence 4, Appli
19	116	96.7	24	US-10-514-653-2	Sequence 2, Appli
20	116	96.7	24	US-10-514-653-19	Sequence 19, Appli
21	111	92.5	24	US-10-514-653-3	Sequence 3, Appli
22	111	92.5	24	US-10-514-653-18	Sequence 18, Appli
23	106	88.3	24	US-10-517-956-6	Sequence 6, Appli
24	106	88.3	24	US-10-514-653-10	Sequence 10, Appli
25	106	88.3	24	US-10-514-653-14	Sequence 14, Appli
26	106	88.3	32	US-10-514-653-16	Sequence 16, Appli
27	103	85.8	21	US-10-306-878-3	Sequence 3, Appli

28	102	85.0	24	US-10-514-653-21	Sequence 21, Appli
29	102	85.0	32	US-10-514-653-22	Sequence 22, Appli
30	88	73.3	17	US-10-514-653-25	Sequence 25, Appli
31	88	73.3	24	US-10-517-956-8	Sequence 8, Appli
32	88	73.3	38	US-10-517-956-7	Sequence 7, Appli
33	87	72.5	24	US-10-481-044-4	Sequence 4, Appli
34	87	72.5	24	US-10-517-956-5	Sequence 5, Appli
35	85	70.8	17	US-10-514-653-13	Sequence 13, Appli
36	84	70.0	17	US-10-514-653-23	Sequence 23, Appli
37	83	69.2	21	US-10-517-956-9	Sequence 9, Appli
38	74	61.7	17	US-10-514-653-11	Sequence 11, Appli
39	59	49.2	41	US-09-925-300-1762	Sequence 1762, Ap
40	48	40.0	60	US-10-425-115-248503	Sequence 248503,
41	47	39.2	175	US-10-437-963-188777	Sequence 188777,
42	46	38.3	152	US-10-029-386-33584	Sequence 33584, A
43	45.5	37.9	181	US-09-864-761-33314	Sequence 33314, A
44	45.5	37.9	181	US-09-864-761-41658	Sequence 41658, A
45	45.5	37.9	181	US-10-029-386-32192	Sequence 32192, A

## ALIGNMENTS

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RESULT 1
US-10-306-878-2
; Sequence 2, Application US/10306878
; Publication No. US20030175819A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods for Identifying Modulators of
; FILE REFERENCE: P-LJ 5535
; CURRENT APPLICATION NUMBER: US/10/306,878
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US 60/334,149
; PRIOR FILING DATE: 2002-11-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-306-878-2

Query Match      100.0%; Score 120; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MAPRGFCLLLTSEIDLPIVKRRA 24
Db      1  MAPRGFCLLLTSEIDLPIVKRRA 24

RESULT 2
US-10-341-434-167
; Sequence 167, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 24
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-341-434-167

Query Match      100.0%; Score 120; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAPRGFSCLLLTSEIDLVPVKRR 24
Db      1 MAPRGFSCLLLTSEIDLVPVKRR 24

RESULT 3
US-10-341-434-200
; Sequence 200, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/346,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/346,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 200
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-200

Query Match      100.0%; Score 120; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAPRGFSCLLLTSEIDLVPVKRR 24
Db      1 MAPRGFSCLLLTSEIDLVPVKRR 24

RESULT 4
US-10-716-432-1
; Sequence 1, Application US/10716432
; Publication No. US2005005620A1
; GENERAL INFORMATION:
; APPLICANT: NOF CORP.
; APPLICANT: NAKAMOTO, Ken-ichiro
; APPLICANT: OHASHI, Syunsuke
; APPLICANT: YAMAMOTO, Yuji
; APPLICANT: SAKANoue, Kenji
; APPLICANT: ITOH, Chika
; APPLICANT: YASUKOCHI, Tohru
; TITLE OF INVENTION: MODIFIED BIO-RELATED SUBSTANCE, PROCESS FOR PRODUCING THE SAME,
; FILE REFERENCE: 078575
; CURRENT APPLICATION NUMBER: US/10/716,432
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: JP 2003-337113
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-716-432-1

Query Match      100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MAPRGFSCLLLTSEIDLVPVKRR 24
Db      1 MAPRGFSCLLLTSEIDLVPVKRR 24

RESULT 5
US-10-852-705A-2
; Sequence 2, Application US/10852705A
; Publication No. US20050191639A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Internationaal Instituut voor Biotechnol
; TITLE OF INVENTION: Method to isolate genes involved in aging
; FILE REFERENCE: RCO/FAC/V098
; CURRENT APPLICATION NUMBER: US/10/852,705A
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: EP01204600.9
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: human HNI cDNA
US-10-852-705A-2

Query Match      100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAPRGFSCLLLTSEIDLVPVKRR 24
Db      1 MAPRGFSCLLLTSEIDLVPVKRR 24

RESULT 6
US-10-517-956-3
; Sequence 3, Application US/10517956
; Publication No. US2005023336A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Novel Screening Method
; FILE REFERENCE: 3067W00P
; CURRENT APPLICATION NUMBER: US/10/517,956
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: JP 2002-173798
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: JP 2002-205470
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 3
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Human
US-10-517-956-3

Query Match      100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAPRGFSCLLLTSEIDLVPVKRR 24
Db      1 MAPRGFSCLLLTSEIDLVPVKRR 24

RESULT 7
US-10-514-653-1
; Sequence 1, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
```

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; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-514-653-1

Query Match          100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPRGFSCLLLTSEIDLPVKRRA 24
Db 1 MAPRGFSCLLLTSEIDLPVKRRA 24

RESULT 8
US-10-514-653-4
; Sequence 4, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: an artificially synthesized polypeptide
; NAME/KEY: MISC FEATURE
; LOCATION: (14)..(14)
; OTHER INFORMATION: The 'Ser' at location 14 stands for phosphorylated Ser.
; US-10-514-653-4

Query Match          100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPRGFSCLLLTSEIDLPVKRRA 24
Db 1 MAPRGFSCLLLTSEIDLPVKRRA 24

RESULT 9
US-10-514-653-5
; Sequence 5, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
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; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: an artificially synthesized polypeptide
; NAME/KEY: MISC FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: The 'Ser' at location 7 stands for phosphorylated Ser.
; US-10-514-653-5

Query Match          100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPRGFSCLLLTSEIDLPVKRRA 24
Db 1 MAPRGFSCLLLTSEIDLPVKRRA 24

RESULT 10
US-10-514-653-6
; Sequence 6, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: an artificially synthesized polypeptide
; NAME/KEY: MISC FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: The 'Ser' at location 7 stands for phosphorylated Ser.
; US-10-514-653-6

Query Match          100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPRGFSCLLLTSEIDLPVKRRA 24
Db 1 MAPRGFSCLLLTSEIDLPVKRRA 24

RESULT 11
US-10-514-653-7
; Sequence 7, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
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; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: an artificially synthesized polypeptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (14)..(14)
; OTHER INFORMATION: The 'Ser' at location 14 stands for D-Ser.
US-10-514-653-7
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Query Match          100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  MAPRGFSCLLLTSEIDLVPVKRR 24
Db      1  MAPRGFSCLLLTSEIDLVPVKRR 24
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RESULT 12
US-10-514-653-8
; Sequence 8, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: an artificially synthesized polypeptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: The 'Ser' at location 7 stands for D-Ser.
US-10-514-653-8
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Query Match          100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  MAPRGFSCLLLTSEIDLVPVKRR 24
Db      1  MAPRGFSCLLLTSEIDLVPVKRR 24
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RESULT 13
US-10-514-653-9
; Sequence 9, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
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; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: an artificially synthesized polypeptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: The 'Ser' at location 7 stands for D-Ser.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (14)..(14)
; OTHER INFORMATION: The 'Ser' at location 14 stands for D-Ser.
US-10-514-653-9
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Query Match          100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  MAPRGFSCLLLTSEIDLVPVKRR 24
Db      1  MAPRGFSCLLLTSEIDLVPVKRR 24
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RESULT 14
US-10-514-653-27
; Sequence 27, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-514-653-27
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Query Match          100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  MAPRGFSCLLLTSEIDLVPVKRR 24
Db      1  MAPRGFSCLLLTSEIDLVPVKRR 24
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RESULT 15
US-10-514-653-17
; Sequence 17, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
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; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 17
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: an artificially synthesized polypeptide
US-10-514-653-17

Query Match      100.0%; Score 120; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 1,1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1  MAPRGFSCLLLTSEIDLPVKRA 24
        |||||||
Db      9  MAPRGFSCLLLTSEIDLPVKRA 32
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Search completed: March 28, 2006, 13:26:03  
Job time : 14.656 secs

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GenCore version 5.1.7  
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3M protein - protein search, using sw model

Run on: March 28, 2006, 13:22:23 ; Search time 1.984 Seconds

(without alignments)  
356.787 Million cell updates/sec

Title: US-10-517-956-3

Perfect score: 120

Sequence: 1 MAPRGFSCLLLTSEIDL PPKRRA 24

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New:\*  
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2: /SIDS5/ptodata/1/pubppaa/US06\_NEW\_PUB.pep.\*  
3: /SIDS5/ptodata/1/pubppaa/US07\_NEW\_PUB.pep.\*  
4: /SIDS5/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep.\*  
5: /SIDS5/ptodata/1/pubppaa/US05\_NEW\_PUB.pep.\*  
6: /SIDS5/ptodata/1/pubppaa/US10\_NEW\_PUB.pep.\*  
7: /SIDS5/ptodata/1/pubppaa/US11\_NEW\_PUB.pep.\*  
8: /SIDS5/ptodata/1/pubppaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	24	US-11-142-255-1	Sequence 1, Appli
2	44	36.7	256	US-11-096-568A-13754	Sequence 13754, A
3	42	35.0	345	US-11-096-568A-356	Sequence 356, App
4	42	35.0	542	US-10-507-755-6	Sequence 6, Appli
5	40.5	33.8	282	US-10-517-939-346	Sequence 346, App
6	40	33.3	24	US-10-895-064-459	Sequence 459, App
7	40	33.3	24	US-11-129-741-459	Sequence 459, App
8	40	33.3	24	US-11-129-741-3477	Sequence 3477, Ap
9	40	33.3	79	US-10-746-909-10	Sequence 10, Appl
10	40	33.3	157	US-10-980-388-73	Sequence 73, Appl
11	40	33.3	157	US-11-087-099-647	Sequence 647, App
12	40	33.3	178	US-10-511-538-85	Sequence 85, Appl
13	40	33.3	194	US-11-087-099-3269	Sequence 3269, Ap
14	39	32.5	44	US-10-467-657-6070	Sequence 6070, Ap
15	39	32.5	74	US-11-123-896-59	Sequence 59, Appl
16	39	32.5	74	US-11-123-896-62	Sequence 62, Appl
17	39	32.5	74	US-11-123-896-65	Sequence 65, Appl
18	39	32.5	74	US-11-123-896-68	Sequence 68, Appl
19	39	32.5	84	US-11-096-568A-4498	Sequence 4498, Ap
20	39	32.5	104	US-11-096-568A-4497	Sequence 4497, Ap
21	39	32.5	189	US-11-107-029-4	Sequence 4, Appli
22	39	32.5	311	US-10-980-388-111	Sequence 111, App
23	39	32.5	311	US-10-980-388-113	Sequence 113, App
24	39	32.5	530	US-10-980-388-62	Sequence 62, Appl
25	39	32.5	689	US-11-087-099-5796	Sequence 5796, Ap

26	39	32.5	691	7	US-11-087-099-5075	Sequence 5075, Ap
27	38.5	32.1	92	7	US-11-096-568A-2284	Sequence 2284, Ap
28	38.5	32.1	95	7	US-11-096-568A-2283	Sequence 2283, Ap
29	38.5	32.1	154	6	US-10-793-626-602	Sequence 602, App
30	38.5	32.1	316	7	US-11-074-176-358	Sequence 358, App
31	38.5	32.1	332	7	US-11-074-176-230	Sequence 230, App
32	38	31.7	121	6	US-10-644-807-410	Sequence 410, App
33	38	31.7	152	7	US-11-096-568A-677	Sequence 677, App
34	38	31.7	152	7	US-11-096-568A-25508	Sequence 25508, A
35	38	31.7	166	7	US-11-096-568A-676	Sequence 676, App
36	38	31.7	166	7	US-11-096-568A-25507	Sequence 25507, A
37	38	31.7	184	7	US-11-096-568A-12134	Sequence 12134, A
38	38	31.7	191	7	US-11-096-568A-675	Sequence 675, App
39	38	31.7	191	7	US-11-096-568A-25506	Sequence 25506, A
40	38	31.7	248	6	US-10-644-807-326	Sequence 326, App
41	38	31.7	250	6	US-10-131-826A-320	Sequence 320, App
42	38	31.7	250	6	US-10-973-115B-320	Sequence 320, App
43	38	31.7	331	7	US-11-185-878-3	Sequence 3, Appli
44	38	31.7	335	7	US-11-182-946-7	Sequence 7, Appli
45	38	31.7	384	7	US-11-087-099-6378	Sequence 6378, Ap

## ALIGNMENTS

RESULT 1  
US-11-142-255-1  
Sequence 1, Application US/11142255  
Publication No. US20050288490A1  
GENERAL INFORMATION:  
APPLICANT: NOF CORP.  
APPLICANT: NAKAMOTO, Ken-ichiro  
APPLICANT: OHASHI, Syunsuke  
APPLICANT: YAMAMOTO, Yuji  
APPLICANT: SAKAMOTO, Kenji  
APPLICANT: ITOH, Chika  
APPLICANT: YASUKOCHI, Tohru  
TITLE OF INVENTION: MODIFIED BIO-RELATED SUBSTANCE, PROCESS FOR PRODUCING THE SAME,  
FILE REFERENCE: 078575  
CURRENT APPLICATION NUMBER: US/11/142,255  
CURRENT FILING DATE: 2005-06-02  
PRIOR APPLICATION NUMBER: US/10/716,432  
PRIOR FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: JP 2003-337113  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1  
LENGTH: 24  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-142-255-1  
Query Match 100.0%; Score 120; DB 7; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.9e-13;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAPRGFSCLLLTSEIDL PPKRRA 24  
Db 1 MAPRGFSCLLLTSEIDL PPKRRA 24  
RESULT 2  
US-11-096-568A-13754  
Sequence 13754, Application US/11096568A  
Publication No. US20060048240A1  
GENERAL INFORMATION:  
APPLICANT: Alexandrov, Nicholas et al.  
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
FILE REFERENCE: 2750-1592PUS2  
CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01  
NUMBER OF SEQ ID NOS: 34471  
SEQ ID NO 13754  
LENGTH: 256  
TYPE: PRT  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(256)  
OTHER INFORMATION: Ceres Seq. ID no. 12355937  
US-11-096-568A-13754

Query Match 36.7%; Score 44; DB 7; Length 256;  
Best Local Similarity 36.4%; Pred. No. 8.2;  
Matches 12; Conservative 8; Mismatches 3; Indels 10; Gaps 2;

Qy 1 MAPRGFSLT-----LITSEIDLPVKRR 24  
Db 163 LSPRDW-CLLRPMQASHLSAQWCLPTRRRA 194

RESULT 3  
US-11-096-568A-356  
Sequence 356, Application US/11096568A  
Publication No. US20060046240A1  
GENERAL INFORMATION:  
APPLICANT: Alexandrov, Nickolai et al.  
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
FILE REFERENCE: 2750-1592PUS2  
CURRENT APPLICATION NUMBER: US/11/096,568A  
CURRENT FILING DATE: 2005-04-01  
NUMBER OF SEQ ID NOS: 34471  
SEQ ID NO 356  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(345)  
OTHER INFORMATION: Ceres Seq. ID no. 15180242  
US-11-096-568A-356

Query Match 35.0%; Score 42; DB 7; Length 345;  
Best Local Similarity 64.3%; Pred. No. 24;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LITSEIDLPVKRR 23  
Db 1 LLPELELPVARR 14

RESULT 4  
US-10-507-755-6  
Sequence 6, Application US/10507755  
Publication No. US20060051754A1  
GENERAL INFORMATION:  
APPLICANT: ENDOU, HITOSHI  
TITLE OF INVENTION: TRANSPORTER SELECTIVELY TRANSPORTING SULFATE CONJUGATE  
FILE REFERENCE: 61552(71526)  
CURRENT APPLICATION NUMBER: US/10/507,755  
CURRENT FILING DATE: 2005-09-14  
PRIOR APPLICATION NUMBER: PCT/JP03/02980  
PRIOR FILING DATE: 2003-03-13  
PRIOR APPLICATION NUMBER: JP 2002-070985  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 6  
LENGTH: 542  
TYPE: PRT

ORGANISM: Homo sapiens  
US-10-507-755-6

Query Match 35.0%; Score 42; DB 6; Length 542;  
Best Local Similarity 72.7%; Pred. No. 39;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FSCLLLTSRI 16  
Db 426 FSCLFLYTSRL 436

RESULT 5  
US-10-517-939-346  
Sequence 346, Application US/10517939  
Publication No. US20060003433A1  
GENERAL INFORMATION:  
APPLICANT: Steer, Brian  
APPLICANT: Callen, Walter  
APPLICANT: Healey, Shaun  
APPLICANT: Hazlewood, Geoff  
APPLICANT: Wu, Di  
APPLICANT: Blum, David  
APPLICANT: Betegehlalian, Alireza  
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM  
FILE REFERENCE: 564462007901  
CURRENT APPLICATION NUMBER: US/10/517,939  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: PCT/US03/19153  
PRIOR FILING DATE: 2003-06-16  
PRIOR APPLICATION NUMBER: 60/389,299  
PRIOR FILING DATE: 2002-06-14  
NUMBER OF SEQ ID NOS: 380  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 346  
LENGTH: 282  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Obtained from an environmental sample.  
US-10-517-939-346

Query Match 33.8%; Score 40.5; DB 6; Length 282;  
Best Local Similarity 50.0%; Pred. No. 34;  
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

Qy 6 FSCLLLTSRI---DLPV 20  
Db 144 FSCLLELVDELLEADVPI 161

RESULT 6  
US-10-895-064-459  
Sequence 459, Application US/10895064  
Publication No. US20060018923A1  
GENERAL INFORMATION:  
APPLICANT: PEIRIS, JOSEPH S.M.  
APPLICANT: YUEN, KWOK YUNG  
APPLICANT: POON, LIT MAN  
APPLICANT: GUAN, YI  
APPLICANT: CHAN, KWOK HUNG  
APPLICANT: NICHOLS, JOHN M.  
APPLICANT: LEUNG, FREDERICK C.  
TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES  
FILE REFERENCE: V0690.0031  
CURRENT APPLICATION NUMBER: US/10/895,064  
CURRENT FILING DATE: 2004-07-21  
NUMBER OF SEQ ID NOS: 2918  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 459  
LENGTH: 24





;; PRIOR FILING DATE: 2000-02-23  
;; PRIOR APPLICATION NUMBER: 60/184,397  
;; PRIOR FILING DATE: 2000-02-23  
;; PRIOR APPLICATION NUMBER: 60/184,247  
;; PRIOR FILING DATE: 2000-02-23  
;; PRIOR APPLICATION NUMBER: 60/188,880  
;; PRIOR FILING DATE: 2000-03-13  
;; PRIOR APPLICATION NUMBER: 60/217,369  
;; PRIOR FILING DATE: 2000-07-11  
;; PRIOR APPLICATION NUMBER: 60/217,370  
;; PRIOR FILING DATE: 2000-07-11  
;; PRIOR APPLICATION NUMBER: 60/218,492  
;; PRIOR FILING DATE: 2000-07-20  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 184  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO: 73  
;; LENGTH: 157  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-980-388-73

Query Match 33.3%; Score 40; DB 6; Length 157;  
Best Local Similarity 53.3%; Pred. No. 22;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 6 FSCLLLTSEIDLPV 20  
Db 30 FKCLLPFSEGMV 44

RESULT 11  
US-11-087-099-647  
;; Sequence 647, Application US/11087099  
;; Publication No. US20060041961A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Abad, Mark S. et al.  
;; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
;; FILE REFERENCE: 38-21(53450)B EP  
;; CURRENT APPLICATION NUMBER: US/11/087,099  
;; CURRENT FILING DATE: 2005-03-22  
;; NUMBER OF SEQ ID NOS: 12464  
;; SEQ ID NO: 647  
;; LENGTH: 157  
;; TYPE: PRT  
;; ORGANISM: Triticum aestivum  
US-11-087-099-647

Query Match 33.3%; Score 40; DB 7; Length 157;  
Best Local Similarity 56.2%; Pred. No. 22;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GFSCLLLTSEIDLPV 20  
Db 41 GFKLLEVLGEMDLPV 56

RESULT 12  
US-10-511-538-85  
;; Sequence 85, Application US/10511538  
;; Publication No. US20060026700A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Oxigene Technologies, Inc  
;; TITLE OF INVENTION: TISSUE SPECIFIC GENES AND GENE CLUSTERS  
;; FILE REFERENCE: 16U 200 PCT  
;; CURRENT APPLICATION NUMBER: US/10/511,538  
;; CURRENT FILING DATE: 2004-10-18  
;; PRIOR APPLICATION NUMBER: US 60/372,669  
;; PRIOR FILING DATE: 2002-04-16  
;; PRIOR APPLICATION NUMBER: US 60/411,882  
;; PRIOR FILING DATE: 2002-09-20  
;; PRIOR APPLICATION NUMBER: US 60/424,336  
;; PRIOR FILING DATE: 2002-11-07

;; PRIOR APPLICATION NUMBER: US 60/374,823  
;; PRIOR FILING DATE: 2002-04-24  
;; PRIOR APPLICATION NUMBER: US 60/376,558  
;; PRIOR FILING DATE: 2002-05-01  
;; PRIOR APPLICATION NUMBER: US 60/381,366  
;; PRIOR FILING DATE: 2002-05-20  
;; PRIOR APPLICATION NUMBER: US 60/403,648  
;; PRIOR FILING DATE: 2002-08-16  
;; NUMBER OF SEQ ID NOS: 344  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO: 85  
;; LENGTH: 178  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-511-538-85

Query Match 33.3%; Score 40; DB 6; Length 178;  
Best Local Similarity 56.2%; Pred. No. 25;  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 9 LLLTSEIDLPVKRA 24  
Db 91 VILLTSELPLVPYRS 106

RESULT 13  
US-11-087-099-3269  
;; Sequence 3269, Application US/11087099  
;; Publication No. US20060041961A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Abad, Mark S. et al.  
;; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
;; FILE REFERENCE: 38-21(53450)B EP  
;; CURRENT APPLICATION NUMBER: US/11/087,099  
;; CURRENT FILING DATE: 2005-03-22  
;; NUMBER OF SEQ ID NOS: 12464  
;; SEQ ID NO: 3269  
;; LENGTH: 194  
;; TYPE: PRT  
;; ORGANISM: Triticum aestivum  
US-11-087-099-3269

Query Match 33.3%; Score 40; DB 7; Length 194;  
Best Local Similarity 56.2%; Pred. No. 28;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GFSCLLLTSEIDLPV 20  
Db 81 GFKLLEVLGEMDLPV 96

RESULT 14  
US-10-467-657-6070  
;; Sequence 6070, Application US/10467657  
;; Publication No. US20050260581A1  
;; GENERAL INFORMATION:  
;; APPLICANT: CHIRON SPA  
;; APPLICANT: FONTANA Maria Rita  
;; APPLICANT: PIZZA Mariagrazia  
;; APPLICANT: MASIGNANI Vega  
;; APPLICANT: MONACI Elisabetta  
;; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
;; FILE REFERENCE:  
;; CURRENT APPLICATION NUMBER: US/10/467,657  
;; CURRENT FILING DATE: 2003-08-11  
;; PRIOR APPLICATION NUMBER: GB-0103424.8  
;; PRIOR FILING DATE: 2001-02-12  
;; NUMBER OF SEQ ID NOS: 9218  
;; SOFTWARE: SeqWin99, version 1.04  
;; SEQ ID NO: 6070  
;; LENGTH: 44  
;; TYPE: PRT  
;; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-6070

Query Match 32.5%; Score 39; DB 6; Length 44;  
Best Local Similarity 50.0%; Pred. No. 8.3;  
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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Db 7 FSCILLLELILKVLKMR 24

RESULT 15

US-11-123-896-59

; Sequence 59, Application US/11123896  
; Publication No. US20050273881A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Navarro Acevedo, Pedro A.  
; APPLICANT: Harvell, Leslie  
; APPLICANT: Cahoon, Rebecca  
; APPLICANT: McCutchen, Billy Fred  
; APPLICANT: Lu, Albert  
; APPLICANT: Herrmann, Rafael  
; TITLE OF INVENTION: Defensein Polynucleotides and Methods of  
; TITLE OF INVENTION: Use  
; FILE REFERENCE: 35718/246703  
; CURRENT APPLICATION NUMBER: US/11/123,896  
; CURRENT FILING DATE: 2005-05-06  
; PRIOR APPLICATION NUMBER: 60/300,152  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 60/300,241  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 469  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 59  
; LENGTH: 74  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-11-123-896-59

Query Match 32.5%; Score 39; DB 7; Length 74;  
Best Local Similarity 55.6%; Pred. No. 15;  
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 5 GFSCLLTSEIDLPVKR 22  
|||:|:|  
Db 7 GFLFLLLVLASDVTVKR 24

Search completed: March 28, 2006, 13:26:39  
Job time : 1.984 secs

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# OM protein - protein search, using sw model

Run on: March 28, 2006, 13:10:18 ; Search time 252.72 Seconds  
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Title: US-10-517-956-1  
Perfect score: 1817  
Sequence: 1 METNFSPTPLNIEYEVSEYSA.....TNDTAANSASPATELQAM 351

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

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Database : A\_Geneseq\_21.\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1817	100.0	351	5	AAU79035 Human for
2	1817	100.0	351	6	ABU89747 Protein d
3	1817	100.0	351	6	ABP81818 Human for
4	1817	100.0	351	7	ADG89689 Human for
5	1817	100.0	351	8	ADH58975 Human GPC
6	1817	100.0	351	8	ADIS5315 Human GPC
7	1817	100.0	351	8	ADO29691 Human GPC
8	1817	100.0	351	8	ADP12531 Protein e
9	1817	100.0	351	8	ADG57846 Human for
10	1817	100.0	351	8	ADP24410 PRO polyp
11	1817	100.0	351	8	ADG74158 Human LXA
12	1817	100.0	351	9	ADK06859 Cyc1in-de
13	1817	100.0	351	9	ADY73233 Human FPR
14	1817	100.0	351	9	AEA27939 Human for
15	1817	100.0	370	6	ABU10071 Human G-P
16	1815	99.9	702	9	ADY73573 Human FPR
17	1811	99.7	351	4	ABBS56354 Non-endog
18	1744	96.0	351	9	ADY73577 Human FPR
19	1725	94.9	351	9	ADY73576 Human FPR
20	1688	92.9	326	6	ABU10072 Human HGP
21	1594	87.7	325	8	ABU10073 Human HGP
22	1420	78.2	351	8	ADH58986 Mouse GPC
23	1420	78.2	351	8	ADIS5333 Mouse FPR
24	1420	78.2	351	8	ADO29714 Mouse GPC

25	1420	78.2	351	8	ADG57850 Mouse for
26	1419	78.1	351	8	ADH58984 Rat GPCR
27	1419	78.1	351	8	ADIS5331 Rat FPR1
28	1419	78.1	351	8	ADG57848 Rat formy
29	1327	73.0	353	5	ABG95152 Human GPC
30	1327	73.0	353	8	ADG64561 Human FPR
31	1327	73.0	413	8	ADG64565 Human N-E
32	1327	73.0	591	7	ADP70495 Orphan re
33	1325	72.9	347	8	ADO29713 Mouse GPC
34	1321	72.7	353	5	ABG95161 Human GPC
35	1321	72.7	353	8	ADG64571 Human FPR
36	1318	72.5	353	6	ABP81729 Human for
37	1318	72.5	353	7	ADD32067 Human for
38	1318	72.5	353	8	ADH58988 Human GPC
39	1318	72.5	353	8	ADIS5335 Human FPR
40	1318	72.5	353	8	ADO29692 Human GPC
41	1318	72.5	353	8	ADP24713 PRO polyp
42	1318	72.5	353	8	ADG17056 Human 155
43	1318	72.5	353	8	ADU01527 Human G P
44	1318	72.5	353	9	ADY73235 Human FPR
45	1316	72.4	353	9	ADY73575 Human FPR

## ALIGNMENTS

RESULT 1	AAU79035	AAU79035 standard; protein; 351 AA.
ID	AAU79035	
AC	AAU79035;	
DT	18-JUN-2002 (first entry)	
XX		
DE	Human formyl peptide receptor like-1 receptor, FPR1-1.	
XX		
KW	Human; FPR1-1; formyl peptide receptor like-1; receptor; ILM receptor;	
KW	macrophage surface receptor; antiinflammatory; pulmonary;	
KW	chronic inflammatory airway disease; chronic bronchitis;	
KW	chronic obstructive pulmonary disease; COPD.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200218938-A1.	
XX		
PD	07-MAR-2002.	
XX		
PF	23-AUG-2001; 2001MO-EP009727.	
XX		
PR	01-SEP-2000; 2000GB-00021484.	
XX		
PA	(BOEH ) BOEHRINGER INGELHEIM PHARMA KG.	
XX		
PI	Jung B, Kraut N, Mueller S, Kistler B, Seither P, Quast K;	
PI	Welch A;	
XX		
DR	WPI; 2002-315580/35.	
XX		
DR	N-PSDB; ABR48101.	
XX		
PT	Determining an expression level of ILM (a macrophage surface receptor),	
PT	for the diagnosis or monitoring of chronic inflammatory airway disease,	
PT	comprises determining the level of the ILM receptor expressed in a	
PT	macrophage.	
XX		
PS	Claim 7; Page 49-51; 79pp; English.	
XX		
CC	The invention relates to determining an expression level of an ILM	
CC	receptor (macrophage surface receptor), comprises determining the level	
CC	of an ILM receptor expressed in a macrophage. Also included are a method	
CC	of determining whether a substance is an activator or an inhibitor of an	
CC	ILM receptor, involving applying the substance to a test system which	
CC	generates a measurable read-out upon modulation of the ILM receptor or an	
CC	ILM receptor function, a test system for determining whether a substance	

CC is an activator or an inhibitor of an ILM receptor function,  
 CC characterised in that the receptor is involved in a chronic inflammatory  
 CC airway disease and where the receptor plays a role in mediating  
 CC inflammation comprising: (i) an ILM receptor; (ii) an expression vector  
 CC capable of expressing an ILM receptor in a cell; or (iii) a host cell  
 CC transformed with an expression vector capable of expressing the ILM  
 CC receptor and a substance determined to be an activator or inhibitor of an  
 CC ILM receptor. The methods are useful for the diagnosis or monitoring of a  
 CC chronic inflammatory airway disease, e.g. chronic bronchitis and chronic  
 CC obstructive pulmonary disease (COPD). The substance determined to be an  
 CC activator or inhibitor of an ILM receptor, is useful for treating the  
 CC diseases and for modulating an ILM receptor in a macrophage. The present  
 CC sequence is an ILM receptor which is differentially expressed and which  
 CC is involved in causing the induction and/or maintenance of the  
 CC hyperactive status of macrophages involved in an inflammatory process

CC  
 XX  
 SQ Sequence 351 AA;

Query Match 100.0%; Score 1817; DB 5; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 7,8e-196;  
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFSPTLNEYBEVSEYASGYTVLRILPLVVLGTVFVLGVGLVWVAGFPMRTTYT 60  
 DB 1 METNFSPTLNEYBEVSEYASGYTVLRILPLVVLGTVFVLGVGLVWVAGFPMRTTYT 60

QY 61 TICVNLALADSFSTATLPFLIVSMAMGEKMPGKFLCKLHIIVDINLFGSVPLIGFIA 120  
 DB 61 TICVNLALADSFSTATLPFLIVSMAMGEKMPGKFLCKLHIIVDINLFGSVPLIGFIA 120

QY 121 LDRICICVLAHVAQNHRVTSIAMKVIYGPWIALVLTLPVFLPTVTIPNGDTYCTENF 180  
 DB 121 LDRICICVLAHVAQNHRVTSIAMKVIYGPWIALVLTLPVFLPTVTIPNGDTYCTENF 180

QY 181 ASNGGTPBERLKVATMTLARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMIKSRPL 240  
 DB 181 ASNGGTPBERLKVATMTLARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMIKSRPL 240

QY 241 RVLTAIVASFFICMPFPQVALIGTWLKMFLFYGKKYKIDILVNPTSLAFNSCLNPM 300  
 DB 241 RVLTAIVASFFICMPFPQVALIGTWLKMFLFYGKKYKIDILVNPTSLAFNSCLNPM 300

QY 301 LYPVVGODFRERLIHSLPTSLERALSDDSAPTNDTAANSASPPATELQAM 351  
 DB 301 LYPVVGODFRERLIHSLPTSLERALSDDSAPTNDTAANSASPPATELQAM 351

RESULT 2  
 ABU89747  
 ID ABU89747 standard; protein; 351 AA.  
 XX  
 AC ABU89747;  
 XX  
 DT 10-JUL-2003 (first entry)  
 XX  
 DE Protein differentially expressed in cardiovascular disease #41.  
 XX  
 KM Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;  
 KM myocardial infarction; candidate; antiarteriosclerotic; antianginal;  
 KM gene therapy; differential gene expression.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W02003031650-A2.  
 XX  
 PD 17-APR-2003.  
 XX  
 PF 02-OCT-2002; 2002WC-EP011034.  
 XX  
 PR 08-OCT-2001; 2001GB-00024145.  
 XX  
 PA (FARB) BAYER AG.  
 XX

PI Munnes M, Gehrmann M, Wick M, Schmitz G;  
 XX  
 DR WPI; 2003-403108/38.  
 DR N-PSDB; ACA89920.  
 XX  
 PT Predicting, diagnosing or prognosing a cardiovascular disease, e.g.  
 PT angina, ischaemia, myocardial infarction or arteriosclerosis by detection  
 PT of a polynucleotide in a biological sample comprises detecting a  
 PT hybridization complex.  
 XX  
 PS Claim 3; Page 375-377; 454pp; English.

CC The invention describes a method of predicting, diagnosing or prognosing  
 CC a cardiovascular disease by detection of a polynucleotide in a biological  
 CC sample comprising hybridizing at least one of the polynucleotide to a  
 CC nucleic acid material of a biological sample, thus forming a  
 CC hybridization complex, and detecting the hybridisation complex. The  
 CC polynucleotides, polypeptides, antisense molecule, antibody and reagent  
 CC are useful for preparing compositions for preventing, predicting or  
 CC diagnosing, or a medicament for treating a cardiovascular disease, e.g.  
 CC arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.  
 CC This sequence represents a protein identified in the invention as being  
 CC differentially expressed in individuals with cardiovascular disease

CC  
 XX  
 SQ Sequence 351 AA;

Query Match 100.0%; Score 1817; DB 6; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 7,8e-196;  
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFSPTLNEYBEVSEYASGYTVLRILPLVVLGTVFVLGVGLVWVAGFPMRTTYT 60  
 DB 1 METNFSPTLNEYBEVSEYASGYTVLRILPLVVLGTVFVLGVGLVWVAGFPMRTTYT 60

QY 61 TICVNLALADSFSTATLPFLIVSMAMGEKMPGKFLCKLHIIVDINLFGSVPLIGFIA 120  
 DB 61 TICVNLALADSFSTATLPFLIVSMAMGEKMPGKFLCKLHIIVDINLFGSVPLIGFIA 120

QY 121 LDRICICVLAHVAQNHRVTSIAMKVIYGPWIALVLTLPVFLPTVTIPNGDTYCTENF 180  
 DB 121 LDRICICVLAHVAQNHRVTSIAMKVIYGPWIALVLTLPVFLPTVTIPNGDTYCTENF 180

QY 181 ASNGGTPBERLKVATMTLARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMIKSRPL 240  
 DB 181 ASNGGTPBERLKVATMTLARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMIKSRPL 240

QY 241 RVLTAIVASFFICMPFPQVALIGTWLKMFLFYGKKYKIDILVNPTSLAFNSCLNPM 300  
 DB 241 RVLTAIVASFFICMPFPQVALIGTWLKMFLFYGKKYKIDILVNPTSLAFNSCLNPM 300

QY 301 LYPVVGODFRERLIHSLPTSLERALSDDSAPTNDTAANSASPPATELQAM 351  
 DB 301 LYPVVGODFRERLIHSLPTSLERALSDDSAPTNDTAANSASPPATELQAM 351

RESULT 3  
 ABP81818  
 ID ABP81818 standard; protein; 351 AA.  
 XX  
 AC ABP81818;  
 XX  
 DT 04-MAR-2003 (first entry)  
 XX  
 DE Human formyl peptide receptor-like receptor protein SEQ ID NO:120.  
 XX  
 KM G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KM G protein-coupled receptor; modulator; antibody; immune-related disease;  
 KM growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KM immunological-related cell proliferative disease; autoimmune disease;  
 KM Alzheimer's disease; arteriosclerosis; infection; osteoarthritis; allergy;  
 KM osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KM graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KM psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KM ulcer.  
 OS Homo sapiens.  
 XX WO200261087-A2.  
 XX 08-AUG-2002.  
 XX 19-DEC-2001; 2001WO-US050107.  
 XX 19-DEC-2000; 2000US-0257144P.  
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
 XX Burner GC, Roush CL, Brown JP;  
 XX WPI; 2003-046718/04.  
 XX N-PSDB; AB242664.  
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.  
 PS Disclosure; Fig 1; 523pp; English.

CC The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related diseases, immunological-related diseases, cell  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention

XX Sequence 351 AA;

Query Match 100.0%; Score 1817; DB 6; Length 351;

Best Local Similarity 100.0%; Pred. No. 7, 8e-196;

Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEEYESYESAGYTVLRILPLVLGVTVFVLGVLGVLVWAGFRMRTVT 60  
 Db 1 METNFTPLNEEYESYESAGYTVLRILPLVLGVTVFVLGVLGVLVWAGFRMRTVT 60  
 QY 61 TITCYLNLADBSFTATLPPLIVSMAMGKMPGWPCKIHIWVDNLGVSFLGFL 120  
 Db 61 TITCYLNLADBSFTATLPPLIVSMAMGKMPGWPCKIHIWVDNLGVSFLGFL 120  
 QY 121 LDRICICVLHVMQNHRTVSLAMKVIQPMILALVLTLPFLFTVTYINGDYCTFNF 180  
 Db 121 LDRICICVLHVMQNHRTVSLAMKVIQPMILALVLTLPFLFTVTYINGDYCTFNF 180  
 QY 181 ASWGGTPEERLKAITMLTARGIIRFVIGFSLPMSIVAICYGLIAKHKKMKISSRPL 240

Db 181 ASWGGTPEERLKAITMLTARGIIRFVIGFSLPMSIVAICYGLIAKHKKMKISSRPL 240  
 QY 241 RVLTAIVASEFFICPFPOVALIGTWLXKEMLFYGYKKIIDIWNPSSLAFNSCLANPM 300  
 Db 241 RVLTAIVASEFFICPFPOVALIGTWLXKEMLFYGYKKIIDIWNPSSLAFNSCLANPM 300  
 QY 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDANSASPAPETELQAM 351  
 Db 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDANSASPAPETELQAM 351

#### RESULT 4

AD C89689  
 ID AD C89689 standard; protein; 351 AA.  
 AC AD C89689;  
 XX 01-JAN-2004 (first entry)  
 DT Human formyl peptide receptor-like 1 (FPR1), SEQ ID NO:2.  
 XX Human formyl peptide receptor-like 1 (FPR1), SEQ ID NO:2.  
 DE Human; formyl peptide receptor-like 1; FPR1; G protein coupled receptor;  
 KM GPCR; drug screening; diagnosis; haematological disease;  
 KM cardiovascular disease; peripheral nervous system disease;  
 KM central nervous system disease; respiratory disease;  
 KM chronic obstructive pulmonary disease; COPD; asthma;  
 KM genito-urological disease; inflammatory disease; neuroprotective;  
 KM cardiac; respiratory; antiasthmatic; antiinflammatory; gene therapy;  
 KM receptor.  
 XX Homo sapiens.  
 OS WO2003082314-A2.  
 XX 09-OCT-2003.  
 PD 21-MAR-2003; 2003WO-EP02959.  
 PF 03-APR-2002; 2002EP-0007291.  
 PR (FAR) BAYER AG.  
 PA Golz S, Brueggemeier U, Geerts A;  
 XX WPI; 2003-803965/75.  
 XX N-PSDB; ADC89688.  
 DR Screening for therapeutic agents for treating a disease e.g.,  
 PT cardiovascular, inflammatory, or respiratory diseases by contacting a  
 PT test compound with a FPR1 polypeptide or polynucleotide and detecting a  
 PT binding of the test compound.  
 XX Disclosure; SEQ ID NO 2; 119pp; English.

XX The invention relates to a method of screening for agents for treating  
 CC formyl peptide receptor-like 1 (FPR1)-related disorders in a mammal. The  
 CC method involves detecting the binding of test compound to an FPR1  
 CC polypeptide or polynucleotide, or determining the activity of an FPR1  
 CC polypeptide at different concentrations of the test compound. FPR1 is a  
 CC G protein coupled receptor (GPCR) which is highly expressed in a variety  
 CC of human tissues. It is expressed in various brain tissues, cardiovascular  
 CC system tissues, erythrocytes and other haematological tissues,  
 CC respiratory tissues, genito-urological tissues such as prostate and  
 CC placenta, and in various immune system tissues. In particular, it is  
 CC expressed at a higher level in lungs affected with chronic obstructive  
 CC pulmonary disease (COPD), compared with healthy lungs. The invention also  
 CC encompasses a method of diagnosing an FPR1-related disorder by  
 CC quantification of FPR1 polynucleotides, and pharmaceutical compositions  
 CC for treating an FPR1-related disorder. Therapeutic agents identified  
 CC using the method of the invention can be used in the treatment of  
 CC disorders such as haematological diseases, cardiovascular diseases,  
 CC peripheral and central nervous system diseases, respiratory diseases

CC (e.g., COPD), asthma, genito-urological diseases, or inflammatory  
 CC diseases. The present sequence represents human FPR1 protein.

XX Sequence 351 AA:

Query Match 100.0%; Score 1817; DB 7; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-196;  
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEYEBVESAGYTVLRILPLVVLGTVFVLGNGLVIMVAGFRMTRTYT 60  
 DB 1 METNFTPLNEYEBVESAGYTVLRILPLVVLGTVFVLGNGLVIMVAGFRMTRTYT 60  
 QY 61 TICYNLALADSFATLPFLIVSMAMGKMPFGMFLCKLHIIVVDINLFGSVFLIGFLA 120  
 DB 61 TICYNLALADSFATLPFLIVSMAMGKMPFGMFLCKLHIIVVDINLFGSVFLIGFLA 120  
 QY 121 LDRICVLHPVMAQNRRVTSIAMKVIYGPWILALVLTLPVFLTLTVTIIPNGDTYCTENF 180  
 DB 121 LDRICVLHPVMAQNRRVTSIAMKVIYGPWILALVLTLPVFLTLTVTIIPNGDTYCTENF 180  
 QY 181 ASWGGTPBERLKVATLMTLARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMIKSSRPL 240  
 DB 181 ASWGGTPBERLKVATLMTLARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMIKSSRPL 240  
 QY 241 RVLTAIVASFFICWPFQVALLGTWMLKEMLFYGYKKIIDILVNPTSSIAFPNSCLNPM 300  
 DB 241 RVLTAIVASFFICWPFQVALLGTWMLKEMLFYGYKKIIDILVNPTSSIAFPNSCLNPM 300  
 QY 301 LVYFVGQDFRERLIHSLPTSLERALSDESAFTNDTAANSASPPATELQAM 351  
 DB 301 LVYFVGQDFRERLIHSLPTSLERALSDESAFTNDTAANSASPPATELQAM 351

# RESULT 5

ID ADH58975 standard; protein; 351 AA.

XX ADH58975;

XX 25-MAR-2004 (first entry)

DE Human GPCR related amino acid sequence #SEQ ID 1.

XX Neotropic; antiparkinsonian; neuroprotective; antidiabetic;  
 KM G-proteorotective; humanin receptor; agonist; antagonist; humanin;  
 KM G-protein coupled receptor protein; GPCR; FPR1; FPR2; nerve; brain;  
 KM Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KM Down's syndrome; prion disease; muscular dystrophy; multiple sclerosis;  
 KM Creutzfeldt-Jacob disease; neuroblastoma.

XX Homo sapiens.

XX WO2003106683-A1.

XX 24-DEC-2003.

XX 12-JUN-2003; 2003WO-JP007500.

XX 14-JUN-2003; 2003JP-00173798.

XX 15-JUL-2003; 2003JP-00205470.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Hinuma S, Fujii R, Harada M, Hosoya M;

XX WPI, 2004-108321/11.

PT Screening potential humanin receptor agonists and antagonists using  
 PT humanin and G-coupled receptor protein FPR1 or FPR2 for apoptosis  
 PT regulation and treatment and prevention of disorders of nerve and brain  
 PT function.

PS Claim 1; SEQ ID NO 1; 160pp; Japanese.

XX The invention relates to a method for screening compounds and their salts  
 CC which modify the binding properties and signal transduction of humanin  
 CC and its salts with humanin receptor protein and its salts, using humanin  
 CC or its salts together with G-protein coupled receptor protein FPR1 or  
 CC FPR2 or its partial peptides or salts or proteins of equivalent  
 CC activity. The method of the invention is useful in the treatment and  
 CC prevention of disorders of nerve and brain function, including  
 CC Alzheimer's disease, Parkinson's disease, Huntington's disease, Down's  
 CC syndrome, prion diseases, muscular dystrophy, diabetic neuropathy,  
 CC multiple sclerosis, cerebral sclerosis, cerebral haemorrhage, cerebral  
 CC ischaemia, subdural hematoma, Creutzfeldt-Jacob disease, neuroblastoma,  
 CC neuropathy associated with viral (including HIV), protozoal or Rickettsia  
 CC infections, and neuropathy associated with vaccination. The current  
 CC sequence represents a human G-protein coupled receptor protein related  
 CC amino acid sequence.

XX Sequence 351 AA:

Query Match 100.0%; Score 1817; DB 8; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-196;  
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEYEBVESAGYTVLRILPLVVLGTVFVLGNGLVIMVAGFRMTRTYT 60  
 DB 1 METNFTPLNEYEBVESAGYTVLRILPLVVLGTVFVLGNGLVIMVAGFRMTRTYT 60  
 QY 61 TICYNLALADSFATLPFLIVSMAMGKMPFGMFLCKLHIIVVDINLFGSVFLIGFLA 120  
 DB 61 TICYNLALADSFATLPFLIVSMAMGKMPFGMFLCKLHIIVVDINLFGSVFLIGFLA 120  
 QY 121 LDRICVLHPVMAQNRRVTSIAMKVIYGPWILALVLTLPVFLTLTVTIIPNGDTYCTENF 180  
 DB 121 LDRICVLHPVMAQNRRVTSIAMKVIYGPWILALVLTLPVFLTLTVTIIPNGDTYCTENF 180  
 QY 181 ASWGGTPBERLKVATLMTLARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMIKSSRPL 240  
 DB 181 ASWGGTPBERLKVATLMTLARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMIKSSRPL 240  
 QY 241 RVLTAIVASFFICWPFQVALLGTWMLKEMLFYGYKKIIDILVNPTSSIAFPNSCLNPM 300  
 DB 241 RVLTAIVASFFICWPFQVALLGTWMLKEMLFYGYKKIIDILVNPTSSIAFPNSCLNPM 300  
 QY 301 LVYFVGQDFRERLIHSLPTSLERALSDESAFTNDTAANSASPPATELQAM 351  
 DB 301 LVYFVGQDFRERLIHSLPTSLERALSDESAFTNDTAANSASPPATELQAM 351

# RESULT 6

ID ADI53315 standard; protein; 351 AA.

XX ADI53315;

XX 22-APR-2004 (first entry)

DE Human FPR1 transmembrane G-protein coupled receptor.

XX screening; binding; signal transduction;  
 KM humanin-like peptide receptor protein; G-protein coupled receptor; FPR1;  
 KM FPR2; transmembrane G-protein coupled receptor; nervous system disorder;  
 KM Alzheimer's disease; Parkinson's disease; Down's syndrome;  
 KM Huntington's disease; muscular dystrophy; prion disease;  
 KM Creutzfeldt-Jacob disease; diabetic neuropathy; multiple sclerosis;  
 KM cerebral ischaemia; apoplexy; brain haemorrhage;  
 KM subarachnoid haemorrhage; human.

XX Homo sapiens.

XX WO2004008141-A1.

XX 22-JAN-2004.



XX 12-JUN-2003; 2003MO-JP007501.  
 XX PF 15-JUL-2002; 2002JP-00205554.  
 XX PA (TAKEDA ) TAKEDA CHEM IND LTD.  
 XX PI Hinuma S, Fujii R, Harada M, Hosoya M, Mori M,  
 XX WPI; 2004-143116/14.  
 XX DR N-PSDB; ADI53316.  
 \*XX PT Screening compounds modifying binding of humanin-like peptide to its  
 PT receptor protein for identification of apoptosis regulators and remedies  
 PT for nervous system disorders, e.g. Alzheimer's disease.  
 XX \*PS Claim 1; SEQ ID NO 1; 116pp; Japanese.  
 XX CC The invention comprises a method for screening for compounds which modify  
 CC the binding or signal transduction of humanin-like peptide receptor  
 CC protein (a G-protein coupled receptor). The method involves the use of  
 CC human, rat or mouse FPR1/FPR2 transmembrane G-protein coupled receptor.  
 CC The compounds isolated by the method of the invention are useful for the  
 CC treatment and prevention of nervous system disorders (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Down's syndrome, Huntington's disease,  
 CC muscular dystrophy, prion disease, Creutzfeldt-Jacob disease, diabetic  
 CC neuropathy, multiple sclerosis, cerebral ischaemia, apoplexy, brain  
 CC haemorrhage and subarachnoid haemorrhage). The present amino acid  
 CC sequence represents a human FPR1 protein.  
 XX SQ Sequence 351 AA;  
 Query Match 100.0%; Score 1817; DB 8; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 7, 8e-196;  
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MERNFSTPLNBYEBSYESAGYVLRLLPLVLTGTVLGVNGVLYWAGRMRTVT 60  
 DB 1 METNFSPLNBYEBSYESAGYVLRLLPLVLTGTVLGVNGVLYWAGRMRTVT 60  
 QY 61 TICYLNALDFSTATLPPLIVSMANGKMPGMPCKLHIVVDNLGSPVLFGEIA 120  
 DB 61 TICYLNALDFSTATLPPLIVSMANGKMPGMPCKLHIVVDNLGSPVLFGEIA 120  
 QY 121 LDRICICVLAHPVMAQNHTVSLAMKVIVGPMIALVLTLPVFLFTVTINBGTCTFNF 180  
 DB 121 LDRICICVLAHPVMAQNHTVSLAMKVIVGPMIALVLTLPVFLFTVTINBGTCTFNF 180  
 QY 121 LDRICICVLAHPVMAQNHTVSLAMKVIVGPMIALVLTLPVFLFTVTINBGTCTFNF 180  
 DB 121 LDRICICVLAHPVMAQNHTVSLAMKVIVGPMIALVLTLPVFLFTVTINBGTCTFNF 180  
 QY 181 ASMGTPBEERLKVATIMLTARGIIRFVIGSLPMSIATCYGLIAKIHKKGMKSSRPL 240  
 DB 181 ASMGTPBEERLKVATIMLTARGIIRFVIGSLPMSIATCYGLIAKIHKKGMKSSRPL 240  
 QY 241 RVLTAVASFFICFPFQVVALGTVLWKMLPFGKRIIDILVNPSSLAFFRSCINPM 300  
 DB 241 RVLTAVASFFICFPFQVVALGTVLWKMLPFGKRIIDILVNPSSLAFFRSCINPM 300  
 QY 301 LYFVGGDFEERLIHSLPTSLERLSDSAFTVDTANASAPPAETELQAM 351  
 DB 301 LYFVGGDFEERLIHSLPTSLERLSDSAFTVDTANASAPPAETELQAM 351  
 RESULT 7  
 ID ADO29691 standard; protein; 351 AA.  
 XX AC ADO29691;  
 XX DT 29-JUL-2004 (first entry)  
 XX XX Human GPCR FPR1, SEQ ID NO:793.  
 XX KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 KW transgenic mouse; neurological disorder; adrenal gland disorder;

KW colon disorder; intestinal disorder; cardiovascular disorder;  
 KW muscular disorder; blood disorder; immune disorder; bone disorder;  
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
 KW kidney disorder; liver disorder; lung disorder; breast disorder;  
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
 KW thymus disorder; thyroid disorder; antiparkinsonian; antineoplastic;  
 KW cytoskeletal; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
 KW CNS; central nervous system; respiratory; antidiabetic; antidiabetic;  
 KW virucide; hepatotropic; antibacterial; antianemic; antiseborrheic;  
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;  
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
 KW receptor.  
 XX OS Homo sapiens.  
 XX PN WO2004040000-A2.  
 XX PD 13-MAY-2004.  
 XX PF 09-SEP-2003; 2003MO-US028226.  
 XX PR 09-SEP-2002; 2002US-0409303P.  
 XX PR 09-APR-2003; 2003US-0461329P.  
 XX PA (PRIM-) PRIMAL INC.  
 XX PI Galtenaxis GA, Bergmann JE, Gragorov A, Hohmann J, Li F,  
 PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;  
 XX WPI; 2004-380329/36.  
 XX DR N-PSDB; ADO30066.  
 XX PT Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.  
 PS Claim 151; SEQ ID NO 793; 542pp; English.  
 XX CC The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising  
 CC probes which hybridize to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders (e.g., autoimmune disorders or  
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the  
 CC invention. Note: The full sequence data for this patent did not form part  
 CC of the printed specification; those sequences not shown were obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 351 AA;

Query Match 100.0%; Score 1817; DB 8; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-196;  
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 METNFSPTLNEYEVESYBSAGYTVLRILPLVVLGVTFLVGLNGLVIVWAGFRMTRTVT 60  
 1 METNFSPTLNEYEVESYBSAGYTVLRILPLVVLGVTFLVGLNGLVIVWAGFRMTRTVT 60  
 1 METNFSPTLNEYEVESYBSAGYTVLRILPLVVLGVTFLVGLNGLVIVWAGFRMTRTVT 60

61 TTCYLNALADPSFTATLPFLIVSMAMGEKMPFGWFLCKLHIIVVDINLFGSVFLIGFIA 120  
 61 TTCYLNALADPSFTATLPFLIVSMAMGEKMPFGWFLCKLHIIVVDINLFGSVFLIGFIA 120  
 61 TTCYLNALADPSFTATLPFLIVSMAMGEKMPFGWFLCKLHIIVVDINLFGSVFLIGFIA 120

121 LDRCTCVLHPVMAQONHRTVSLAMKVIVGPMILALVTLVPFLFTVTTPNGDTCTFNF 180  
 121 LDRCTCVLHPVMAQONHRTVSLAMKVIVGPMILALVTLVPFLFTVTTPNGDTCTFNF 180  
 121 LDRCTCVLHPVMAQONHRTVSLAMKVIVGPMILALVTLVPFLFTVTTPNGDTCTFNF 180

181 ASWGGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVAICYGLIAKIHKKMKISRPL 240  
 181 ASWGGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVAICYGLIAKIHKKMKISRPL 240  
 181 ASWGGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVAICYGLIAKIHKKMKISRPL 240

241 RVLTAIVASFFICWPFQVALIGTWLAKEMLFYGYKKIIDILVNPTSLAFNSCLNPM 300  
 241 RVLTAIVASFFICWPFQVALIGTWLAKEMLFYGYKKIIDILVNPTSLAFNSCLNPM 300  
 241 RVLTAIVASFFICWPFQVALIGTWLAKEMLFYGYKKIIDILVNPTSLAFNSCLNPM 300

301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDPAANSASPPAETELQAM 351  
 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDPAANSASPPAETELQAM 351  
 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDPAANSASPPAETELQAM 351

RESULT 8  
 ADP12531  
 ID ADP12531 standard; protein; 351 AA.  
 XX  
 AC ADP12531;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Protein encoded by mRNA of the invention #141.  
 XX  
 KW transplanted rejection; immune system; rheumatoid arthritis; lupus;  
 XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004042346-A2.  
 XX  
 PD 21-MAY-2004.  
 XX  
 PF 24-APR-2003; 2003WO-US012946.  
 XX  
 PR 24-APR-2002; 2002US-00131831.  
 XX  
 PR 20-DEC-2002; 2002US-00325899.  
 XX  
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
 XX  
 PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;  
 PI Rosenberg S;  
 XX  
 DR WPI; 2004-400724/37.  
 XX  
 PA Diagnosing or monitoring transplanted rejection, e.g. heart, kidney, liver,  
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplanted  
 PT rejection, in an individual, comprises detecting the expression level of  
 PT the genes.  
 XX  
 PS Claim 65; SEQ ID NO 2540; 1762bp; English.  
 XX  
 CC The present invention relates to diagnosing or monitoring transplanted  
 CC rejection, e.g. cardiac or kidney transplanted rejection, in an individual  
 CC comprising detecting the expression level of one or more genes. The  
 CC method, system and kits are useful in diagnosing or monitoring  
 CC transplanted rejection, e.g. heart, kidney, liver, pancreas, pancreatic

CC islet, lung, bone marrow or stem cell transplanted rejection,  
 CC xenotransplanted rejection or mechanical organ replacement rejection, in an  
 CC individual. The method is also useful in assessing the immune status of  
 CC an individual. The methods are also useful in diagnosing and monitoring  
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,  
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or  
 CC viral, bacterial or fungal infection. The present sequence represents a  
 CC protein that is encoded by the mRNA of the invention.  
 XX

Sequence 351 AA;  
 SQ

Query Match 100.0%; Score 1817; DB 8; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-196;  
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 METNFSPTLNEYEVESYBSAGYTVLRILPLVVLGVTFLVGLNGLVIVWAGFRMTRTVT 60  
 1 METNFSPTLNEYEVESYBSAGYTVLRILPLVVLGVTFLVGLNGLVIVWAGFRMTRTVT 60  
 1 METNFSPTLNEYEVESYBSAGYTVLRILPLVVLGVTFLVGLNGLVIVWAGFRMTRTVT 60

61 TTCYLNALADPSFTATLPFLIVSMAMGEKMPFGWFLCKLHIIVVDINLFGSVFLIGFIA 120  
 61 TTCYLNALADPSFTATLPFLIVSMAMGEKMPFGWFLCKLHIIVVDINLFGSVFLIGFIA 120  
 61 TTCYLNALADPSFTATLPFLIVSMAMGEKMPFGWFLCKLHIIVVDINLFGSVFLIGFIA 120

121 LDRCTCVLHPVMAQONHRTVSLAMKVIVGPMILALVTLVPFLFTVTTPNGDTCTFNF 180  
 121 LDRCTCVLHPVMAQONHRTVSLAMKVIVGPMILALVTLVPFLFTVTTPNGDTCTFNF 180  
 121 LDRCTCVLHPVMAQONHRTVSLAMKVIVGPMILALVTLVPFLFTVTTPNGDTCTFNF 180

181 ASWGGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVAICYGLIAKIHKKMKISRPL 240  
 181 ASWGGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVAICYGLIAKIHKKMKISRPL 240  
 181 ASWGGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVAICYGLIAKIHKKMKISRPL 240

241 RVLTAIVASFFICWPFQVALIGTWLAKEMLFYGYKKIIDILVNPTSLAFNSCLNPM 300  
 241 RVLTAIVASFFICWPFQVALIGTWLAKEMLFYGYKKIIDILVNPTSLAFNSCLNPM 300  
 241 RVLTAIVASFFICWPFQVALIGTWLAKEMLFYGYKKIIDILVNPTSLAFNSCLNPM 300

301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDPAANSASPPAETELQAM 351  
 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDPAANSASPPAETELQAM 351  
 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDPAANSASPPAETELQAM 351

RESULT 9  
 ADOS7846  
 ID ADOS7846 standard; peptide; 351 AA.  
 XX  
 AC ADOS7846;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Human formyl peptide receptor-like 1 SEQ ID NO:2.  
 XX  
 KW antiaesthetic; antiallergic; antiinflammatory; antiarteriosclerotic;  
 KW neuroprotective; antianxiety; cerebroprotective; antianesthetic; virucide;  
 KW antinfertive; immunomodulator; asthma; allergic disease; inflammation;  
 KW arteriosclerosis; FPR1; formyl peptide receptor-like 1; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004041850-A1.  
 XX  
 PD 21-MAY-2004.  
 XX  
 PF 06-NOV-2003; 2003WO-JP014138.  
 XX  
 PR 07-NOV-2002; 2002JP-00324189.  
 XX  
 PR 18-DEC-2002; 2002JP-00367119.  
 XX  
 PR 05-MAR-2003; 2003JP-00059073.  
 XX  
 PR 03-JUL-2003; 2003JP-00191359.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Hinuma S, Kobayashi M, Habata Y, Harada M, Okubo S, Yoshida H;  
 PI Nishi K;  
 XX

DR WPI; 2004-400641/37.  
 DR N-PSDB; AD057847.  
 XX  
 XX G protein-coupled receptor protein FPR1, its ligands, encoded  
 PT polynucleotides and antibodies for diagnosis and screening drugs for e.g.  
 PT asthma, allergic diseases, inflammations and arteriosclerosis.  
 XX  
 PS Claim 25; SEQ ID NO 2; 191pp; Japanese.  
 XX  
 XX The invention relates to a novel peptide containing an amino acid  
 CC sequence identical or substantially similar to that of AD057845 or  
 CC AD057865 with 13 or 15 amino acids, respectively, in which the N-terminal  
 CC methionine is optionally formulated, its amide, ester or their salt. A  
 CC peptide of the invention has antiasthmatic, antiallergic,  
 CC antiinflammatory, antiarteriosclerotic, neuroprotective, antianginal,  
 CC cerebroprotective, antinaemic, virucide, antineurotic, and  
 CC immunomodulator activity. The receptor protein, its ligands, their  
 CC encoded polynucleotides and antibodies are useful in the diagnosis of and  
 CC screening drugs for e.g. asthma, allergic diseases, inflammations and  
 CC arteriosclerosis. With these ligands, agonists and antagonists can be  
 CC efficiently screened. An endogenous FPR1 (formyl peptide receptor-1) like  
 CC 1) ligand P3 was purified from pig's stomach after extraction and  
 CC chromatography for characterisation. Cloning of a rat spleen-originated  
 CC FPR1-encoded cDNA was also performed, and the clone was used in  
 CC constructing an expression vector and other biotechnological  
 CC manipulations as well as biological evaluation. The present sequence  
 CC represents human FPR1.  
 CC  
 XX Sequence 351 AA:  
 SQ  
 Query Match 100.0%; Score 1817; DB 8; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 7,8e-196;  
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 METNFSPTPLNBYEVEVSAGYTVLRILPLVVGTVFVGLNGLVYVWAGFRMRTVT 60  
 DB 1 METNFSPTPLNBYEVEVSAGYTVLRILPLVVGTVFVGLNGLVYVWAGFRMRTVT 60  
 QY 61 TICVNLALADFSFTATLPPLIVSMAMGKMPGFWPLCKLIHVVDINLFGSVFLGFIA 120  
 DB 61 TICVNLALADFSFTATLPPLIVSMAMGKMPGFWPLCKLIHVVDINLFGSVFLGFIA 120  
 QY 121 LDRICVLAHPVMAQNHRVTSIAKVIIGVPIALVLTLPVFLPTVTIIPNGDYYCTFNF 180  
 DB 121 LDRICVLAHPVMAQNHRVTSIAKVIIGVPIALVLTLPVFLPTVTIIPNGDYYCTFNF 180  
 QY 181 ASWNGTPEERLKAIVTMLTARGIIRPVIGSLPMSIYALCYGLIAAKIHKKGMKSSRPL 240  
 DB 181 ASWNGTPEERLKAIVTMLTARGIIRPVIGSLPMSIYALCYGLIAAKIHKKGMKSSRPL 240  
 QY 241 RVLTAAVASPFICWFPFQVALAGTVMKEMLFYGKTKIIDILVNPSSLAFFNSCLNPM 300  
 DB 241 RVLTAAVASPFICWFPFQVALAGTVMKEMLFYGKTKIIDILVNPSSLAFFNSCLNPM 300  
 QY 301 LVYFVGQDFRRLIHSPLTSLERALSBDSPNTDNTAANSAPPAETELQAM 351  
 DB 301 LVYFVGQDFRRLIHSPLTSLERALSBDSPNTDNTAANSAPPAETELQAM 351  
 RESULT 10  
 ADP24410  
 ID ADP24410 standard; protein; 351 AA.  
 XX  
 XX ADP24410;  
 DT 18-NOV-2004 (first entry)  
 DE PRO polypeptide SEQ ID NO:1588.  
 XX  
 XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;  
 KM osteopathic; antidiabetic; dermatological; antipneumatic; antiallergic;  
 KM antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.  
 XX

OS Unidentified.  
 XX  
 XX WO2004041170-A2.  
 XX  
 XX 21-MAY-2004.  
 PD  
 XX  
 XX 30-OCT-2003; 2003WO-US034312.  
 PF  
 XX  
 XX 01-NOV-2002; 2002US-0423394P.  
 PR  
 XX  
 XX (GERTH ) GENENTECH INC.  
 PA  
 XX  
 XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;  
 PI Wu TD;  
 DR WPI; 2004-419628/39.  
 DR N-PSDB; ADP24409.  
 XX  
 XX New PRO polypeptides and polynucleotides, useful for treating e.g.  
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated  
 PT renal disease, or demyelinating diseases of the central or peripheral  
 PT nervous system.  
 XX  
 XX Claim 7; SEQ ID NO 1588; 2940pp; English.  
 XX  
 XX The invention relates to a novel isolated nucleic acid and the PRO  
 CC polypeptide encoded by it. A protein of the invention has  
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,  
 CC osteopathic, antidiabetic, dermatological, antipneumatic, antiallergic,  
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide  
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its  
 CC agonist, antagonist, or antibody that specifically binds to the  
 CC polypeptide is useful for treating an immune related disorder such as  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 CC disease, a demyelinating disease of the central or peripheral nervous  
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,  
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary  
 CC disease, infectious or autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food  
 CC hypersensitivity, urticaria, an immunologic disease of the lung,  
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
 CC pneumonitis, a transplantation associated disease, graft rejection or  
 CC graft-versus-host disease. The present sequence represents a PRO protein  
 CC of the invention.  
 XX  
 XX Sequence 351 AA:  
 SQ  
 Query Match 100.0%; Score 1817; DB 8; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 7,8e-196;  
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 METNFSPTPLNBYEVEVSAGYTVLRILPLVVGTVFVGLNGLVYVWAGFRMRTVT 60  
 DB 1 METNFSPTPLNBYEVEVSAGYTVLRILPLVVGTVFVGLNGLVYVWAGFRMRTVT 60  
 QY 61 TICVNLALADFSFTATLPPLIVSMAMGKMPGFWPLCKLIHVVDINLFGSVFLGFIA 120  
 DB 61 TICVNLALADFSFTATLPPLIVSMAMGKMPGFWPLCKLIHVVDINLFGSVFLGFIA 120  
 QY 121 LDRICVLAHPVMAQNHRVTSIAKVIIGVPIALVLTLPVFLPTVTIIPNGDYYCTFNF 180  
 DB 121 LDRICVLAHPVMAQNHRVTSIAKVIIGVPIALVLTLPVFLPTVTIIPNGDYYCTFNF 180  
 QY 181 ASWNGTPEERLKAIVTMLTARGIIRPVIGSLPMSIYALCYGLIAAKIHKKGMKSSRPL 240  
 DB 181 ASWNGTPEERLKAIVTMLTARGIIRPVIGSLPMSIYALCYGLIAAKIHKKGMKSSRPL 240

DB 181 ASWGTPBERLKYAITMLTARGIIRFVIGSLPMSIVAICYGLIAKHKGMKISRRL 240  
 QY 241 RVLTAIVASFFICWPFQVALLGTWVKEMLPYGKXKIIDILVNPSTSLAFNSCLNPM 300  
 DB 241 RVLTAIVASFFICWPFQVALLGTWVKEMLPYGKXKIIDILVNPSTSLAFNSCLNPM 300  
 QY 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPATNDTAANSASPPAETELQAM 351  
 DB 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPATNDTAANSASPPAETELQAM 351

RESULT 11  
 ADS74158  
 ID ADS74158 standard; protein; 351 AA.  
 AC ADS74158;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Human LXA4 receptor.  
 XX  
 KM Human; Reso E receptor 1; LXA4; antiinflammatory;  
 KM G-protein coupled receptor; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 122..142  
 FT /note="Second intracellular loop"  
 FT Domain 287..309  
 FT /note="Transmembrane domain 7"  
 XX  
 PN MO2004078143-A2.  
 XX  
 PD 16-SEP-2004.  
 XX  
 PF 05-MAR-2004; 2004WO-US006766.  
 XX  
 PR 05-MAR-2003; 2003US-0452244P.  
 XX  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
 XX  
 PI Serhan CN, Arita M;  
 XX  
 DR WPI; 2004-662347/64.  
 XX  
 PT Screening candidate substance for anti-inflammatory activity; involves  
 PT connecting cell expressing Reso E receptor with candidate substance, and  
 PT detecting biological activity mediated by Reso E receptor.  
 XX  
 PS Disclosure; Fig 3; 33pp; English.  
 XX  
 CC The present sequence is that of the human LXA4 receptor (ALX), a G-  
 CC protein coupled receptor (GPCR). The invention is based, in part, on the  
 CC recognition that resolvin E1 receptor (Reso E1) shares similar  
 CC structural features to LO-derived eicosanoid receptors such as the LXA4  
 CC receptor. A claimed method of identifying a receptor that mediates an  
 CC antiinflammatory activity of a resolvin substance comprises: introducing a  
 CC nucleic acid configured to express a GPCR into a cell that does not  
 CC endogenously produce the GPCR; contacting the cell with a substance  
 CC comprising a resolvin; and detecting that the cell has a reduced cytokine  
 CC induced activation of a NF-kB transcription factor relative to a cell not  
 CC contacted by the substance. A claimed method for screening a candidate  
 CC substance for antiinflammatory activity comprises detecting that the  
 CC candidate substance alters an activity mediated by a GPCR. The GPCR  
 CC preferably has sequence identity within the second intracellular loop or  
 CC 7th transmembrane domain of human ALX.  
 XX  
 SQ Sequence 351 AA;  
 Query Match 100.0%; Score 1817; DB 8; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 7,8e-196;  
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFSPTLNEYBEVSEBSAGTIVTILPLVVLGTVLGVLGNGLVIVAGFRMTRVTT 60  
 DB 1 METNFSPTLNEYBEVSEBSAGTIVTILPLVVLGTVLGVLGNGLVIVAGFRMTRVTT 60  
 QY 61 TTCYLNALADPSFATLTPFLIVSNMAGRKWPGWFLCKLHHVVDINLFGSVFLIGFTA 120  
 DB 61 TTCYLNALADPSFATLTPFLIVSNMAGRKWPGWFLCKLHHVVDINLFGSVFLIGFTA 120  
 QY 121 LDRICVLHPVMAQNRRVTSIAMKVIQGPWIIALVLTLPVPLFTVTTIPNGDYCTFNF 180  
 DB 121 LDRICVLHPVMAQNRRVTSIAMKVIQGPWIIALVLTLPVPLFTVTTIPNGDYCTFNF 180  
 QY 181 ASWGTPBERLKYAITMLTARGIIRFVIGSLPMSIVAICYGLIAKHKGMKISRRL 240  
 DB 181 ASWGTPBERLKYAITMLTARGIIRFVIGSLPMSIVAICYGLIAKHKGMKISRRL 240  
 QY 241 RVLTAIVASFFICWPFQVALLGTWVKEMLPYGKXKIIDILVNPSTSLAFNSCLNPM 300  
 DB 241 RVLTAIVASFFICWPFQVALLGTWVKEMLPYGKXKIIDILVNPSTSLAFNSCLNPM 300  
 QY 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPATNDTAANSASPPAETELQAM 351  
 DB 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPATNDTAANSASPPAETELQAM 351

RESULT 12  
 ADX06859  
 ID ADX06859 standard; protein; 351 AA.  
 AC ADX06859;  
 XX  
 DT 21-APR-2005 (first entry)  
 XX  
 DB Cyclin-dependent kinase modulation biomarker SEQ ID NO 1424.  
 XX  
 KM cytostatic; cyclin-dependent kinase; cdk; biomarker.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO2005012875-A2.  
 XX  
 PD 10-FEB-2005.  
 XX  
 PF 29-JUL-2004; 2004WO-US024424.  
 XX  
 PR 29-JUL-2003; 2003US-0490890P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;  
 XX  
 DR WPI; 2005-163068/17.  
 DR N-PsDB; ADX06858.  
 PT Biomarkers useful for predicting or determining the response of a mammal  
 PT to a cancer treatment comprising administration of a modulator of cyclin-  
 PT dependent kinase activity.  
 XX  
 PS Claim 5; SEQ ID NO 1424; 141pp; English.  
 XX  
 CC This invention describes a novel method of predicting or determining  
 CC whether a mammal will respond or is responding to an anti-cancer agent  
 CC that modulates cyclin-dependent kinase (cdk) activity. The method  
 CC comprises measuring the level of one or more biomarkers selected from  
 CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID  
 CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the  
 CC invention is utilized in a kit for determining or predicting whether  
 CC patient would be susceptible or resistant to treatment by an agent  
 CC modulating cdk activity. The invention also describes a method for  
 CC utilizing individualized genetic profiles for treating diseases and  
 CC disorders based on patient's response and molecular level, specialized  
 CC microarrays comprising the biomarkers described, antibodies directed

CC against the biomarkers and a cell culture model to identify biomarkers.  
 CC The cdk modulator is preferably N-5-[(5-(1,1-Dimethyl-2-oxazolyl)methyl)thio]-2-chiazolyl-4-piperidine carboxamide, 0.5-L-tartaric acid salt. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fcp.wipo.int/pub/published\_pat\_sequences. This CC sequence represents a biomarker used in the method of the invention.

CC Sequence 351 AA;

Query Match 100.0%; Score 1817; DB 9; Length 351;

Best Local Similarity 100.0%; Pred. No. 7.8e-196;

Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEXEYESAGYTVLRILPLVVGTVFVGLNGGLVIVWAGFRMTRTYT 60  
 DB 1 METNFTPLNEXEYESAGYTVLRILPLVVGTVFVGLNGGLVIVWAGFRMTRTYT 60  
 QY 61 TICYMLALADFSFTATLPFLIVSMAGKMPGFWFLCKLHIIVVDINLFGSVFLIGFTA 120  
 DB 61 TICYMLALADFSFTATLPFLIVSMAGKMPGFWFLCKLHIIVVDINLFGSVFLIGFTA 120  
 QY 121 LDRCTCVLHPWMAQNRRVSLAMKYVGGPWIALVTLTPFLTLTYTTPNGDTCTFNF 180  
 DB 121 LDRCTCVLHPWMAQNRRVSLAMKYVGGPWIALVTLTPFLTLTYTTPNGDTCTFNF 180  
 QY 181 ASWGTPEERLKVATMLTARGIIRFVIGSLPMSIVAICYGLIAKHKKGIKSSRPL 240  
 DB 181 ASWGTPEERLKVATMLTARGIIRFVIGSLPMSIVAICYGLIAKHKKGIKSSRPL 240  
 QY 241 RVLTAIVASFFTCWPFQVALLGTWMLKEMLFYGYKXIIDLIVNPTSSLAFFNSCLNPM 300  
 DB 241 RVLTAIVASFFTCWPFQVALLGTWMLKEMLFYGYKXIIDLIVNPTSSLAFFNSCLNPM 300  
 QY 301 LYFVQODFRERLIHSLPTSLERALSDBSAPTNDTAANSAPPAETELQAM 351  
 DB 301 LYFVQODFRERLIHSLPTSLERALSDBSAPTNDTAANSAPPAETELQAM 351

RESULT 13

ID ADY73233 standard; protein; 351 AA.

XX AC ADY73233;

DT 02-JUN-2005 (first entry)

XX DE Human PPR1.

XX neuroprotective; nootropic; gene therapy; substrate inhibition;

KW gene expression; diagnosis; Alzheimer's disease; neuroprotective;

KW nootropic; degeneration; neurological disease; cognitive disorder; PPR1;

XX receptor.

OS Homo sapiens.

XX WO2005024057-A1.

XX PD 17-MAR-2005.

PF 10-SEP-2003; 2003WO-EP010160.

PR 10-SEP-2003; 2003WO-EP010160.

XX (GALA-) GALAPAGOS GENOMICS NV.

PI Merchiers PG, Splittels KF, Hoffmann M, Thys K, Laenen W;

DR WPI; 2005-233298/24.

PT Identifying compound that changes amyloid beta precursor protein processing in cell; involves exposing cell to compound; comparing activity level of polypeptide before and after exposing cell to compound;

PT and identifying compound.

XX Example 2; Fig 8; 86pp; English.

CC The invention describes a method of identifying (M1) a compound that changes the amyloid-beta precursor protein processing in a cell, involving providing a host cell expressing a polypeptide having one of 14 amino acid sequences (SEQ ID No. 15-28), determining activity level of polypeptide, exposing the host cell to a compound, determining activity level of the polypeptide, and identifying the compound, by which the second activity level is less than the first activity level. Also described are: changing the amyloid-beta precursor protein processing of a cell; a polynucleotide (I) comprising a nucleotide sequence chosen from one of 310 fully defined 21 base pair sequences (SEQ ID No. 29-338) given in the specification; a vector (II) comprising (I); and diagnosing a pathological condition involving cognitive impairment or a susceptibility to the condition in a subject. (M1) is useful for identifying a compound that changes the amyloid-beta precursor protein processing in a cell. (I) or (II) is useful as a medicament or for producing medicament for treating a disease (e.g. Alzheimer's disease) involving cognitive impairment. This is the amino acid sequence of human receptor PPR1 associated with the reduction of GPCR expression and subsequent inhibition of amyloid beta production. Note: The invention claims SEQ ID No 8 1-28 which are not shown in the specification.

CC Sequence 351 AA;

Query Match 100.0%; Score 1817; DB 9; Length 351;

Best Local Similarity 100.0%; Pred. No. 7.8e-196;

Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEXEYESAGYTVLRILPLVVGTVFVGLNGGLVIVWAGFRMTRTYT 60  
 DB 1 METNFTPLNEXEYESAGYTVLRILPLVVGTVFVGLNGGLVIVWAGFRMTRTYT 60  
 QY 61 TICYMLALADFSFTATLPFLIVSMAGKMPGFWFLCKLHIIVVDINLFGSVFLIGFTA 120  
 DB 61 TICYMLALADFSFTATLPFLIVSMAGKMPGFWFLCKLHIIVVDINLFGSVFLIGFTA 120  
 QY 121 LDRCTCVLHPWMAQNRRVSLAMKYVGGPWIALVTLTPFLTLTYTTPNGDTCTFNF 180  
 DB 121 LDRCTCVLHPWMAQNRRVSLAMKYVGGPWIALVTLTPFLTLTYTTPNGDTCTFNF 180  
 QY 181 ASWGTPEERLKVATMLTARGIIRFVIGSLPMSIVAICYGLIAKHKKGIKSSRPL 240  
 DB 181 ASWGTPEERLKVATMLTARGIIRFVIGSLPMSIVAICYGLIAKHKKGIKSSRPL 240  
 QY 241 RVLTAIVASFFTCWPFQVALLGTWMLKEMLFYGYKXIIDLIVNPTSSLAFFNSCLNPM 300  
 DB 241 RVLTAIVASFFTCWPFQVALLGTWMLKEMLFYGYKXIIDLIVNPTSSLAFFNSCLNPM 300  
 QY 301 LYFVQODFRERLIHSLPTSLERALSDBSAPTNDTAANSAPPAETELQAM 351  
 DB 301 LYFVQODFRERLIHSLPTSLERALSDBSAPTNDTAANSAPPAETELQAM 351

RESULT 14

ID AEA27939 standard; protein; 351 AA.

XX AC AEA27939;

DT 28-JUL-2005 (first entry)

XX DE Human formyl peptide receptor-like 1.

XX Formyl peptide receptor-like 1; Lipoxin A4 receptor;

KW rheumatoid arthritis; immune disorder; inflammation;

KW musculoskeletal disease; antiarthritic; antiinflammatory;

KW Alzheimer's disease; neurological disease; degeneration; nootropic; neuroprotective; asthma; antiasthmatic; respiratory disease; trauma; vulnary; injury; radiation injuries; antileptic; cytostatic; renal disease; nephrotropic; endocrine disease; genitourinary disease;

glomerular disease; cardiovascular disease; hypertension; hypotensive;  
myocardial infarction; cardiatic; myocardial ischemia; vasotropic;  
allergy; anti-allergic; immune disorder; shock; gout; antigout;  
musculoskeletal disease; psoriasis; antipsoriatic;  
dermatological disease; allergic; rhinitis; ear; nose; throat disease;  
respiratory distress syndrome; respiratory-gen.; respiratory disease;  
Crohn's disease; gastroenteric-gen.; gastrointestinal disease;  
hemorrhagic shock; endotoxic shock; glomerular disease;  
benign prostatic hypertrophy; neoplasm; inflammatory bowel disease;  
brain injury; cerebroprotective; systemic lupus erythematosus;  
metabolic disorder; vasoconstriction; pain; analgesic; diabetes;  
antidiabetic; bacterial infection; antibacterial; viral infection;  
viricide; cancer.

Homo sapiens.  
MO2005047899-A2.

26-MAY-2005.

04-NOV-2004; 2004MO-US036952.

07-NOV-2003; 2003US-0518476P.  
10-NOV-2003; 2003US-0519085P.  
30-JUL-2004; 2004US-0592926P.

(ACAD-) ACADIA PHARM INC.

Nash N, Scully AL, Gardell L, Olsson R, Gustafsson M;  
WPI, 2005-395823/40.  
N-PSDB; AEA27938.

Use of lipoxin receptor as screening tool to identify compounds effective  
in treating inflammation and associated pain.

Claim 5; SEQ ID NO 2; 75bp; English.

The present sequence is the protein sequence of human formyl peptide  
receptor-like 1 (FPR1), also known as lipoxin A4 receptor. The invention  
relates to the use of the FPR1 as a tool to identify compounds effective  
in treating inflammation and associated pain, and to the use of such  
compounds as therapeutics. A method of screening for a compound able to  
affect one or more activities of a FPR1 receptor comprises: (a)  
contacting a recombinant cell with a test compound, where the recombinant  
cell comprises a recombinant nucleic acid expressing FPR1 (provided the  
cell does not have endogenous FPR1 expression); and (b) determining the  
ability of the test compound to affect one or more activities of FPR1. A  
compound that activates a FPR1 receptor subtype is used in a claimed  
method for treating acute and chronic inflammation, such as inflammation  
associated with diabetes, viral infection, irritable bowel syndrome,  
amputation, cancer, bacterial infection, physical injury, including  
physical trauma and radiation exposure, vasoconstriction as a result of  
asthma, anaphylactic reactions, allergic reactions, shock, diabetes,  
rheumatoid arthritis, gout, psoriasis, allergic rhinitis, adult  
respiratory distress syndrome, Crohn's disease, endotoxin shock,  
traumatic shock, hemorrhagic shock, bowel ischemic shock, renal  
glomerular disease, benign prostatic hypertrophy, myocardial ischemia,  
myocardial infarction, circulatory shock, brain injury including ischemic  
stroke and hemorrhagic stroke, systemic lupus erythematosus, chronic  
renal disease, cardiovascular disease and hypertension or chemical injury  
(all claimed). Also claimed are: cells that express FPR1 receptor, which  
are used in a claimed method of identifying agonists of FPR1; a method  
of treating inflammation, where the inflammatory response results from  
the activation of leukocytes and comprises leukocyte migration and  
generation of reactive oxygen species to evoke vascular leakage or edema,  
is associated with rheumatoid arthritis, Alzheimer's disease or asthma,  
results from physical injury, including physical trauma and radiation  
exposure; a method of inducing vasodilation to treat or prevent a  
vasoconstrictive response or condition such as renal hemodynamic disease,  
including glomerular disease, a cardiovascular disease, including  
hypertension, myocardial infarction and myocardial ischemia; and a method  
for antagonizing a vasoconstrictive response to a sulfideptide

leukotriene in a subject, where the response is a renal vasoconstrictive  
response including mild vasoconstriction such as chronic renal disease  
and chronic severe vasoconstriction such as glomerular kidney disease.

Sequence 351 AA;  
Query Match 100.0%; Score 1817; DB 9; Length 351;  
Best Local Similarity 100.0%; Pred. No. 7.8e-196;  
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 METNFSPTPLNXYEVEVSAGYTVLRILPLVYLGVTVLGVNGLVIMVAGFRMRTVT 60  
1 METNFSPTPLNXYEVEVSAGYTVLRILPLVYLGVTVLGVNGLVIMVAGFRMRTVT 60  
61 TICYNLALADSPFATLPFLIVSMAGKMPGWLCTLIHIVVDINLFGSVFLIGFLA 120  
61 TICYNLALADSPFATLPFLIVSMAGKMPGWLCTLIHIVVDINLFGSVFLIGFLA 120  
121 LDRCTCVLHPVMAQNRHTVSLAMKVIVGWIILALVITLTPVPLFTVTITPNQDTYCTENF 180  
121 LDRCTCVLHPVMAQNRHTVSLAMKVIVGWIILALVITLTPVPLFTVTITPNQDTYCTENF 180  
121 LDRCTCVLHPVMAQNRHTVSLAMKVIVGWIILALVITLTPVPLFTVTITPNQDTYCTENF 180  
181 ASWGTPEERLKVATIMLTARGLIRPVIGSLPMSIVATCYGLIAKIHKKGISSRPL 240  
181 ASWGTPEERLKVATIMLTARGLIRPVIGSLPMSIVATCYGLIAKIHKKGISSRPL 240  
241 RVLTAIVASFFICWPFQVALIGTWMLEKMLFYGKYKIIDILVNPTSSLAFFNSCLNPM 300  
241 RVLTAIVASFFICWPFQVALIGTWMLEKMLFYGKYKIIDILVNPTSSLAFFNSCLNPM 300  
301 LVYVGGQDRERLIHSLPISLRALSEDSAPFNVDPAANSASPAPTELOAM 351  
301 LVYVGGQDRERLIHSLPISLRALSEDSAPFNVDPAANSASPAPTELOAM 351

RESULT 15  
ABU10071  
ID ABU10071 standard; protein; 370 AA.  
XX  
AC ABU10071;  
XX  
DT 15-AUG-2003 (first entry)  
XX  
DE Human G-protein coupled receptor HGPBRMY39.  
XX  
KW Human; receptor; G-protein coupled receptor; HGPBRMY39; cancer;  
KW male reproductive disorder; testicular disorder; immune disorder;  
KW inflammatory disorder; developmental disorder; leukemia;  
KW bone marrow disorder; testicular cancer; proliferative disorder;  
KW neural disorder; Alzheimer's disease; prion disorder;  
KW bone metabolism disorder.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 2..370  
FT /note="This region is claimed in claim 5"  
XX  
PN MO2003023007-A2.  
XX  
XX 20-MAR-2003.  
PD  
XX 06-SEP-2002; 2002WO-US028582.  
PF  
XX 07-SEP-2001; 2001US-0317793P.  
PR  
XX 27-NOV-2001; 2001US-0333658P.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
PI Ramanathan CS, Gopal S, Mintler G, Feder JN;  
XX WPI, 2003-313245/30.  
DR N-PSDB; ACA61401.

XX New human G-protein coupled receptor, HGPBMY39, useful for treating or  
PT preventing e.g. immune, inflammatory, developmental, proliferative,  
PA neural, reproductive, bone marrow or prion disorders.

PS Claim 5, Fig 1, 359pp, English.

XX The invention relates to an isolated nucleic acid encoding a human G-  
CC protein coupled receptor HGPBMY39 (or its fragment domain or epitope),  
CC its complement or a polynucleotide capable of hybridising under stringent  
CC conditions to it. Also included are a HGPBMY39 recombinant vector, a  
CC recombinant host cell comprising the vector sequences (used to express  
CC and make the protein), an isolated HGPBMY39 polypeptide, and an anti-  
CC HGPBMY39 antibody. The HGPBMY39 polynucleotides and polypeptide is  
CC useful for preventing, treating or ameliorating e.g. a (male)  
CC reproductive disorder; a testicular disorder or cancer; a disorder  
CC related to aberrant G-protein coupled signalling, particularly N-formyl  
CC peptide receptor dependent signalling; a disorder related to aberrant G-  
CC protein coupled receptor dependent phosphatidylinositol-calcium  
CC signalling; a disorder related to aberrant G-protein couple receptor  
CC dependent phosphatidylinositol or calcium second messenger activation; an  
CC immune disorder; an inflammatory disorder; a developmental disorder; a  
CC disorder that would benefit from inhibition of a leukotriene B4-dependent  
CC proinflammatory signal; aberrant N-formyl peptide signalling; aberrant  
CC neutrophil activation; a disorder associated with hyper neutrophil  
CC activation; a disorder associated with below normal neutrophil activation  
CC ; a disorder related to aberrant intracellular and/or extracellular  
CC oxidation states; a disorder related to aberrant superoxide generation;  
CC leukaemia; a bone marrow disorder; cancer; proliferative disorders;  
CC neural disorders; a disorder related to aberrant neutrophil chemotaxis;  
CC Alzheimer's disease; prion disorders; and a bone metabolism disorder. The  
CC present sequence represents HGPBMY39

XX  
SQ Sequence 370 AA;

Query Match 100.0%; Score 1817; DB 6; Length 370;  
Best Local Similarity 100.0%; Pred. No. 8.4e-196;  
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFSPTLNEYEVSYESAGYTLRLPLVVLGVTVLGVNGGLVYTWAGPRMTRVT 60  
DB 20 METNFSPTLNEYEVSYESAGYTLRLPLVVLGVTVLGVNGGLVYTWAGPRMTRVT 79  
QY 61 TICYNIALADFSPTATLPFLIVSMANGKMPFCMLIHIVVDINLFGSVFLIGFIA 120  
DB 80 TICYNIALADFSPTATLPFLIVSMANGKMPFCMLIHIVVDINLFGSVFLIGFIA 139  
QY 121 LDRICVLAHPVMAQNHTVSLAMKVIQVPIALVLTLPVFLPTVTIPNGDYCTENF 180  
DB 140 LDRICVLAHPVMAQNHTVSLAMKVIQVPIALVLTLPVFLPTVTIPNGDYCTENF 199  
QY 181 ASWGGTPEERLKAITMLTARGIIRFYIGSLPMSIYACGLIAAKIHKKGMKSRPL 240  
DB 200 ASWGGTPEERLKAITMLTARGIIRFYIGSLPMSIYACGLIAAKIHKKGMKSRPL 259  
QY 241 RVLTAVASPFICMPFQVALIGTWLXKMLPYGKYKIIDILVNPSSLAFFNSCLNPM 300  
DB 260 RVLTAVASPFICMPFQVALIGTWLXKMLPYGKYKIIDILVNPSSLAFFNSCLNPM 319  
QY 301 LYYFVGODPFRERLIHSLPTSLERALSBSAFTNDTANASAPPAETELQAM 351  
DB 320 LYYFVGODPFRERLIHSLPTSLERALSBSAFTNDTANASAPPAETELQAM 370

Search completed: March 28, 2006, 13:14:57  
Job time : 254.22 secs

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CC disease, Huntington's disease, cerebropinal ataxia and familial  
 CC amyotrophic lateral sclerosis  
 XX  
 SQ Sequence 24 AA;

Query Match 100.0%; Score 120; DB 4; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGFSCLLLTSEIDL PVKRR 24  
 |||||  
 DB 1 MARGFSCLLLTSEIDL PVKRR 24

RESULT 2  
 AAB81835  
 ID AAB81835 standard; peptide; 24 AA.  
 XX  
 AC AAB81835;  
 XX  
 DT 06-JUN-2001 (first entry)  
 XX

DE Nerve cell death inhibition method related peptide SEQ ID NO: 5.

XX Alzheimer's disease; nerve cell death; APP variant; presenilin variant;  
 KM humanin.  
 XX

OS Homo sapiens.

PN WO200121787-A1.

XX

PD 29-MAR-2001.

XX 14-SEP-2000; 2000MO-JF006314.

PR 17-SEP-1999; 99JP-00264679.

XX 29-JUN-2000; 2000JP-00201456.  
 (UYKE-) UNIV KEIO.

PA Nishimoto I;

XX WPI; 2001-290433/30.

DR N-PSDB; AAF81621.

XX

PT Humanin peptides which inhibits cell death useful for treatment of

XX Alzheimer's and other nervous system diseases.

PS Example 1; Page 94; 116pp; Japanese.

XX

CC The present invention provides humanin peptides which inhibit cell death

CC associated with Alzheimer's disease. They can be used in the treatment of

XX Alzheimer's disease and as models for the development of new drugs useful

CC in treating the same

XX

SQ Sequence 24 AA;

Query Match 100.0%; Score 120; DB 4; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGFSCLLLTSEIDL PVKRR 24  
 |||||  
 DB 1 MARGFSCLLLTSEIDL PVKRR 24

RESULT 3  
 ABB44628  
 ID ABB44628 standard; peptide; 24 AA.  
 XX  
 AC ABB44628;  
 XX  
 DT 07-FEB-2002 (first entry)

XX Human protective sequence CNI-00734 peptide #5.

XX Human; protective sequence; cell death; cancer; autoimmune disease;  
 KM neurological disorder; stroke; cytostatic; neuroprotective; gene therapy.

XX Homo sapiens.

PN WO200176457-A2.

XX 18-OCT-2001.

XX 09-APR-2001; 2001MO-US011663.

XX 11-APR-2000; 2000US-00547735.

XX (COGE-) COGENT NEUROSCIENCE INC.

PA Thomas MB, Portbury SD, Puranam K, Katz LC, Lo DC, Barney S;

XX WPI; 2002-025874/03.

DR N-PSDB; ABA82707.

XX

PT New protective sequences and their products, useful for diagnosing and

XX treating diseases involving cell death, including neurological disorders

XX e.g. stroke and for identifying modulators of expression of the

XX protective sequences.

XX Claim 1; Fig 4; 283pp; English.

XX The present invention relates to protective sequence proteins (ABB44624-

CC ABB44830) and their coding sequences (ABA82701-ABA82937). The sequences,

CC when introduced into a cell either predisposed to undergo cell death or

CC in the process of undergoing cell death, prevent, delay or rescue the

CC cell from death, hence, these sequences are named "protective sequences".

CC The sequences are useful for treating and/or ameliorating cancer.

CC autoimmune diseases and neurological disorders e.g. stroke. Further

CC examples of diseases which may be treated by the present invention are

CC given in the specification

XX Sequence 24 AA;

Query Match 100.0%; Score 120; DB 5; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGFSCLLLTSEIDL PVKRR 24  
 |||||  
 DB 1 MARGFSCLLLTSEIDL PVKRR 24

RESULT 4  
 AAU73274  
 ID AAU73274 standard; peptide; 24 AA.  
 XX  
 AC AAU73274;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX

DE Human protective DNA sequence CNI-00736 open reading frame #5.  
 XX Human; protective sequence; cell death; central nervous system; stroke;  
 KM ischaemia; open reading frame; ORF; cerebral herniation; septic embolism;  
 KM cerebral oedema; meningitis; protozoal infection; malaria; CNI-00733;  
 KM metazoal infection; vascular disease; eye; macular degeneration; trauma;  
 KM diabetic retinopathy; epidural haematoma; tumour; degenerative disease;  
 KM nutritional condition; environmental condition; metabolic condition;  
 KM CNI-00736; CNI-00738; CNI-00742; CNI-00748; cancer; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200181361-A1.  
 XX

PD 01-NOV-2001.  
XX  
PF 09-APR-2001; 2001WO-US011501.  
XX  
PR 11-APR-2000; 2000US-00547938.  
XX  
PA (COGE-) COGENT NEUROSCIENCE INC.  
XX  
PI Portbury SD, Purnam K, Katz LC, Lo DC, Barney S, Thomas MB;  
XX  
DR MPI: 2002-066433/09.  
XX N-PSTDB; MAS98431.  
PT Polypeptides and polynucleotides comprising protective sequences useful  
PT for preventing, delaying or rescuing a cell from death in disease,  
PT condition or disorders such as Alzheimer's disease, stroke, tumors,  
PT trauma.  
XX  
PS Claim 17; Fig 5F; 228bp; English.

The invention relates to an isolated polypeptide encoded by a protective sequence, which is a polynucleotide comprising sequences which when introduced into a cell either predisposed to undergo cell death or in the process of undergoing cell death, prevent, delay, or rescue the cell from death, relative to a corresponding cell into which exogenous nucleic acids have been introduced. The sequences of the invention are useful for diagnosing a protective sequence-mediated condition, disorder or disease in an individual. The treatable disorders are preferably of the central nervous system of humans including ischaemia-related conditions such as stroke, cerebral herniation, septic embolism, cerebral oedema, infections such as meningitis, protozoal infections such as malaria, metazoal infections such as echinococcosis, vascular diseases such as ischaemic encephalopathy, conditions involving the eye such as macular degeneration, diabetic retinopathy, trauma such as epidural haematoma, tumours such as primary intracranial tumours, degenerative diseases such as Alzheimer's disease and nutritional, environmental and metabolic conditions. Sequences AUV73255-AUV73378 represent open reading frames of the human protective sequence polynucleotides

SQ Sequence 24 AA;

Query Match 100.0%; Score 120; DB 5; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MAPRGFSCLLLTSTRIIDLPVKRRRA 24  
|||||  
Db 1 MAPRGFSCLLLTSTRIIDLPVKRRRA 24

RESULT 5  
AU69614 standard; protein; 24 AA.  
ID AU69614 standard; protein; 24 AA.  
AC  
AAU69614;  
DT 30-JAN-2002 (first entry)  
DS Cell death protective sequence CNI-00725, protein #4.  
DE  
Human; protective sequence; cell death; cerebral oedema; infection;  
meningitis; degenerative disease; Alzheimer's disease; heart disease;  
motor neuron disease; demyelinating disease; multiple sclerosis; asthma;  
nutritional condition; peripheral nervous system disorder; ischaemia;  
diabetic neuropathy; autoimmune haemolytic anaemia; respiratory system;  
oral cavity; gastrointestinal tract; liver; cirrhosis; pancreatitis;  
polycystic renal disease; urinary tract; genitalia; endometriosis;  
breast; chronic mastitis; thyroid gland; Hashimoto's thyroiditis;  
adrenal gland; skin; psoriasis; muscular atrophy; bone marrow;  
osteoporosis; cancer; autoimmune disease.  
KW Homo sapiens.  
XX

PW	MO200176532-A2.
XX	
PD	18-OCT-2001.
XX	
PF	09-APR-2001; 2001WO-US011655.
XX	
PR	11-APR-2000; 2000US-00547596.
XX	
PA	(COGE-) COGENT NEUROSCIENCE INC.
PI	Barney S, Thomas MB, Portbury SD, Putnam K, Katz LC, Lo DC;
DR	WPI; 2002-017408/02.
DR	N-Psdb; AAS63013.
XX	
PT	Novel nucleic acids referred as protective sequences and their encoded
PT	products for diagnosing, treating diseases involving cell death,
PT	including neurological disorders e.g. stroke and for identifying
PT	modulators.
XX	
PS	Claim 17; Fig 6D; 256pp; English.
XX	
CC	The invention relates to isolated protective sequence polypeptides (I)
CC	and polynucleotides (II). (II) is useful for transferring a protective
CC	sequence into a cell, which delays and/or prevents the cell from
CC	undergoing cell death. Protective sequences, their products or antibodies
CC	are useful diagnostically, prophylactically, therapeutically or as
CC	targets for treatment and diagnosis of conditions, disorders or diseases
CC	involving cell death. The protective sequences and their products are
CC	useful for preventing or creating disorders of the central nervous system
CC	including neurological and psychiatric conditions, cerebral oedema,
CC	infections such as meningitis, degenerative diseases such as Alzheimer's
CC	and motor neuron disease, demyelinating diseases such as multiple
CC	sclerosis, nutritional conditions, disorders of the peripheral nervous
CC	system including diabetic neuropathy, disorders which cause cell death in
CC	organ systems including blood vessels, heart (ischaemia), blood cells
CC	(autoimmune haemolytic anaemia), respiratory system (asthma), oral
CC	cavity, gastrointestinal tract, liver (cirrhosis), pancreatitis,
CC	polycystic renal disease, urinary tract, genitalia (congenital
CC	anomalies), endometriosis, breast (chronic mastitis), thyroid gland
CC	(Hashimoto's thyroiditis), adrenal gland, skin (psoriasis),
CC	muculoskeletal system (muscular atrophy), bone marrow or bone
CC	(osteoporosis). The compositions promote cell death and are useful for
CC	treating and/or ameliorating cancer and autoimmune diseases. The
CC	compounds are further useful for treating physiological impacts on organs
CC	caused by infection which induce cell death. (I) is useful to raise an
CC	immune response, as a reagent in assays designed to quantitatively
CC	determine levels of the protein in biological fluids, as markers for
CC	tissues in which the corresponding protein is expressed and to isolate
CC	receptors or ligands. AAU69571-AAU69736 represent the protective
CC	polypeptide sequences as described in the invention
XX	
SQ	Sequence 24 AA;
OY	
DB	Query Match 100.0%; Score 120; DB 5; Length 24; Best Local Similarity 100.0%; Pred. No. 1,3e-12; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1	MARPGFSLLLITSEIDL PVKRRRA 24       
1	MARPGFSLLLITSEIDL PVKRRRA 24       
RESULT 6	
AAO30161	
ID	AAO30161 standard; peptide; 24 AA.
XX	
AC	AAO30161;
XX	
DT	03-SEP-2003 (first entry)
XX	
DE	Human humanin protein, HNI.
XX	

KM Human; aging-associated disease; oxidative stress; AAD; HNL; humanin.  
 XX Homo sapiens.  
 OS WO2003045988-A2.  
 XX  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 28-NOV-2002; 2002WO-EP013549.  
 XX  
 PR 29-NOV-2001; 2001BP-00204600.  
 XX  
 PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
 XX  
 XX Contreras RH; Chen C;  
 PI  
 DR WPI; 2003-505183/47.  
 XX N-PSDB; AAL60805.  
 DR  
 XX Screening genes involved in aging and/or aging-associated diseases or in  
 PT oxidative stress by mutating and cultivating a yeast cell, enriching the  
 PT population, labeling the mother cells and isolating the highly labeled  
 PT cells.  
 PS Claim 13; Page 38; 78pp; English.  
 XX  
 CC The invention relates to a method for screening genes involved in aging  
 CC and/or aging-associated diseases (AAD) or in oxidative stress. The method  
 CC involves mutating and cultivating a yeast cell, enriching the population  
 CC for mother cells, labeling the mother cells and isolating the highly  
 CC labelled cells. The present sequence is human humanin protein, HNL. This  
 CC sequence is used to illustrate the method of the invention  
 CC  
 XX  
 SQ Sequence 24 AA;  
 Query Match 100.0%; Score 120; DB 6; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-12; Indels 0; Gaps 0;  
 Matches 24; Conservative 0; Mismatches 0;  
 QY 1 MAPRGFSCLLLTSEIDLPVKRRR 24  
 Db 1 MAPRGFSCLLLTSEIDLPVKRRR 24  
 RESULT 7  
 AAO30314  
 ID AAO30314 standard; peptide; 24 AA.  
 XX  
 AC AAO30314;  
 XX  
 DT 22-SEP-2003 (first entry)  
 XX  
 DE Human humanin (cytosolic form) peptide.  
 XX  
 XX Humanin; bax; bcl; therapy; Alzheimer's disease; Parkinson's disease;  
 KW neuron cell death; cancer; autoimmune disorder; nootropic; vasodilator;  
 KW anticonvulsant; tranquillizer; vulnerary; cardiant; antiinflammatory;  
 KW stroke; Huntington's disease; trauma; amyotrophic lateral sclerosis;  
 KW human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003046205-A2.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 27-NOV-2002; 2002WO-US038191.  
 XX  
 PR 28-NOV-2001; 2001US-0334149P.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 XX Reed JC, Guo B;  
 PI

XX WPI; 2003-505209/47.  
 DR N-PSDB; AAL61053.  
 XX  
 XX Identifying modulators of apoptosis, in particular binding modulators of  
 PT humanin to bax or bcl, useful for diagnosing and/or treating disorders  
 PT such as Alzheimer's disease, Parkinson's disease, cancer and inflammatory  
 PT disorders.  
 PS Disclosure; Fig 3B; 141pp; English.  
 XX  
 CC The invention relates to method for identifying an effective compound  
 CC that modulates the binding of humanin to bax and/or bcl. The method is  
 CC useful for diagnosing and/or treating disorders associated with the  
 CC humanin-bax or humanin-bcl complex, such as Alzheimer's disease, stroke,  
 CC Parkinson's disease, Huntington's disease, trauma, amyotrophic lateral  
 CC sclerosis, neuron cell death, cancer or inflammatory or autoimmune  
 CC disorders. The present sequence is human humanin (cytosolic form)  
 CC peptide. This sequence is used to illustrate the method of the invention  
 CC  
 XX  
 SQ Sequence 24 AA;  
 Query Match 100.0%; Score 120; DB 7; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-12; Indels 0; Gaps 0;  
 Matches 24; Conservative 0; Mismatches 0;  
 QY 1 MAPRGFSCLLLTSEIDLPVKRRR 24  
 Db 1 MAPRGFSCLLLTSEIDLPVKRRR 24  
 RESULT 8  
 ADF95055  
 ID ADF95055 standard; peptide; 24 AA.  
 XX  
 AC ADF95055;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Humanin peptide derivative P-S14 HN.  
 XX  
 KW HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;  
 KW Alzheimer's disease.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 14 /note="phosphorylated"  
 XX  
 XX WO2003097687-A2.  
 PN  
 PD 27-NOV-2003.  
 XX  
 PF 16-MAY-2003; 2003WO-JP006139.  
 XX  
 PR 16-MAY-2002; 2002US-0380958P.  
 XX  
 XX (NISH/) NISHIMOTO I.  
 PA  
 XX Nishimoto I;  
 PT  
 DR WPI; 2004-061983/06.  
 XX  
 PT New Humanin derivative that protects a neuronal cell from cytotoxicity,  
 PT useful for treating neurodegenerative disorders (e.g. Alzheimer's  
 PT disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated  
 PT amino acid.  
 XX  
 PS Claim 8; SEQ ID NO 4; 82pp; English.  
 XX  
 CC The invention relates to a derivative of humanin (HN) that protects a

CC neuronal cell from cytotoxicity, where the derivative contains at least  
CC one D-amino acid or phosphorylated amino acid, or where the derivative  
CC has an addition of one or more amino acids having an activity of forming  
CC a multimer. The humanin derivatives are useful in protecting neuronal  
CC cells from cytotoxicity related to neurodegenerative diseases. The  
-CC composition and method are useful in treating neurodegenerative  
CC disorders, such as Alzheimer's disease. The present sequence represents a  
CC HN peptide derivative.  
XX  
SQ Sequence 24 AA;  
Query Match 100.0%; Score 120; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAPRGFSCLLLTSEIDLPIVGRRA 24  
DB 1 MAPRGFSCLLLTSEIDLPIVGRRA 24  
RESULT 9  
ADPF95059  
ID ADF95059 standard; peptide: 24 AA.  
XX  
AC ADF95059;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Humanin peptide derivative D-Ser7 HN.  
XX  
KW HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;  
KW Alzheimer's disease.  
XX  
OS Synthetic.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Misc-difference 7 /note= "D-form residue"  
PN WO2003097687-A2.  
XX  
PD 27-NOV-2003.  
XX  
PF 16-MAY-2003; 2003WO-JP006139.  
XX  
PR 16-MAY-2002; 2002US-0380958P.  
PA (NISH/) NISHIMOTO I.  
XX  
PI Nishimoto I;  
XX  
DR WPI; 2004-061983/06.  
XX  
PT New Humanin derivative that protects a neuronal cell from cytotoxicity,  
PT useful for treating neurodegenerative disorders (e.g. Alzheimer's  
PT disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated  
PT amino acid.  
XX  
XX  
PS Claim 8; SEQ ID NO 8; 82pp; English.  
XX  
CC The invention relates to a derivative of humanin (HN) that protects a  
CC neuronal cell from cytotoxicity, where the derivative contains at least  
CC one D-amino acid or phosphorylated amino acid, or where the derivative  
CC has an addition of one or more amino acids having an activity of forming  
CC a multimer. The humanin derivatives are useful in protecting neuronal  
CC cells from cytotoxicity related to neurodegenerative diseases. The  
CC composition and method are useful in treating neurodegenerative  
CC disorders, such as Alzheimer's disease. The present sequence represents a  
CC HN peptide derivative.  
XX  
SQ Sequence 24 AA;

Query Match 100.0%; Score 120; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAPRGFSCLLLTSEIDLPIVGRRA 24  
DB 1 MAPRGFSCLLLTSEIDLPIVGRRA 24  
RESULT 10  
ADPF95060  
ID ADF95060 standard; peptide: 24 AA.  
XX  
AC ADF95060;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Humanin peptide derivative D-Ser7/14 HN.  
XX  
KW HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;  
KW Alzheimer's disease.  
XX  
OS Synthetic.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Misc-difference 7 /note= "D-form residue"  
FT Misc-difference 14 /note= "D-form residue"  
PN WO2003097687-A2.  
XX  
PD 27-NOV-2003.  
XX  
PF 16-MAY-2003; 2003WO-JP006139.  
XX  
PR 16-MAY-2002; 2002US-0380958P.  
PA (NISH/) NISHIMOTO I.  
XX  
PI Nishimoto I;  
XX  
DR WPI; 2004-061983/06.  
XX  
PT New Humanin derivative that protects a neuronal cell from cytotoxicity,  
PT useful for treating neurodegenerative disorders (e.g. Alzheimer's  
PT disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated  
PT amino acid.  
XX  
XX  
PS Claim 8; SEQ ID NO 9; 82pp; English.  
XX  
CC The invention relates to a derivative of humanin (HN) that protects a  
CC neuronal cell from cytotoxicity, where the derivative contains at least  
CC one D-amino acid or phosphorylated amino acid, or where the derivative  
CC has an addition of one or more amino acids having an activity of forming  
CC a multimer. The humanin derivatives are useful in protecting neuronal  
CC cells from cytotoxicity related to neurodegenerative diseases. The  
CC composition and method are useful in treating neurodegenerative  
CC disorders, such as Alzheimer's disease. The present sequence represents a  
CC HN peptide derivative.  
XX  
SQ Sequence 24 AA;  
Query Match 100.0%; Score 120; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAPRGFSCLLLTSEIDLPIVGRRA 24  
DB 1 MAPRGFSCLLLTSEIDLPIVGRRA 24

```

RESULT 11
ADP95052
XX ID ADF95052 standard; peptide; 24 AA.
XX AC ADF95052;
XX DT 26-FEB-2004 (first entry)
XX DE Humanin (HN) wild-type peptide sequence.
XX KM HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;
XX KW Alzheimer's disease.
XX OS Homo sapiens.
XX PN WO2003097687-A2.
XX PD 27-NOV-2003.
XX PF 16-MAY-2003; 2003WO-JP006139.
XX PR 16-MAY-2002; 2002US-0380958P.
XX PA (NISH/) NISHIMOTO I.
XX PI Nishimoto I;
XX PS WPI; 2004-061983/06.
XX DR N-PSDB; ADP95077.
XX PT New Humanin derivative that protects a neuronal cell from cytotoxicity,
XX PT useful for treating neurodegenerative disorders (e.g. Alzheimer's
XX PT disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
XX PT amino acid.
XX PS Example 1; SEQ ID NO 1; 82pp; English.
XX XX
XX CC The invention relates to a derivative of humanin (HN) that protects a
XX CC neuronal cell from cytotoxicity, where the derivative contains at least
XX CC one D-amino acid or phosphorylated amino acid, or where the derivative
XX CC has an addition of one or more amino acids having an activity of forming
XX CC a multimer. The humanin derivatives are useful in protecting neuronal
XX CC cells from cytotoxicity related to neurodegenerative diseases. The
XX CC composition and method are useful in treating neurodegenerative
XX CC disorders, such as Alzheimer's disease. The present sequence represents a
XX CC HN wild-type peptide sequence.
XX SQ Sequence 24 AA;
XX
XX Query Match 100.0%; Score 120; DB 8; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-12;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MAPRGFSCLLLTSEIDLPIVKRRA 24
XX DB 1 MAPRGFSCLLLTSEIDLPIVKRRA 24
XX
XX RESULT 12
ADP95057
XX ID ADF95057 standard; peptide; 24 AA.
XX AC ADF95057;
XX XX
XX DT 26-FEB-2004 (first entry)
XX DE Humanin peptide derivative P-S7/14 HN.
XX KM HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;
XX KW Alzheimer's disease.
XX OS Synthetic.
XX OS Homo sapiens.
XX

```

```

XX XX
XX FH Key Location/Qualifiers
XX FT Modified-site 7 /note="phosphorylated"
XX FT FT Modified-site 14 /note="phosphorylated"
XX FT FT /note="phosphorylated"
XX PN WO2003097687-A2.
XX PD 27-NOV-2003.
XX PF 16-MAY-2003; 2003WO-JP006139.
XX PR 16-MAY-2002; 2002US-0380958P.
XX PA (NISH/) NISHIMOTO I.
XX PI Nishimoto I;
XX PS WPI; 2004-061983/06.
XX DR N-PSDB; ADP95077.
XX PT New Humanin derivative that protects a neuronal cell from cytotoxicity,
XX PT useful for treating neurodegenerative disorders (e.g. Alzheimer's
XX PT disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
XX PT amino acid.
XX PS Example 1; SEQ ID NO 6; 82pp; English.
XX XX
XX CC The invention relates to a derivative of humanin (HN) that protects a
XX CC neuronal cell from cytotoxicity, where the derivative contains at least
XX CC one D-amino acid or phosphorylated amino acid, or where the derivative
XX CC has an addition of one or more amino acids having an activity of forming
XX CC a multimer. The humanin derivatives are useful in protecting neuronal
XX CC cells from cytotoxicity related to neurodegenerative diseases. The
XX CC composition and method are useful in treating neurodegenerative
XX CC disorders, such as Alzheimer's disease. The present sequence represents a
XX CC HN peptide derivative.
XX SQ Sequence 24 AA;
XX
XX Query Match 100.0%; Score 120; DB 8; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-12;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MAPRGFSCLLLTSEIDLPIVKRRA 24
XX DB 1 MAPRGFSCLLLTSEIDLPIVKRRA 24
XX
XX RESULT 13
ADP95056
XX ID ADF95056 standard; peptide; 24 AA.
XX AC ADF95056;
XX XX
XX DT 26-FEB-2004 (first entry)
XX DE Humanin peptide derivative P-S7 HN.
XX KM HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;
XX KW Alzheimer's disease.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Modified-site 7 /note="phosphorylated"
XX FT FT /note="phosphorylated"
XX PN WO2003097687-A2.
XX PD 27-NOV-2003.
XX

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PF 16-MAY-2003; 2003WO-JP006139.  
XX  
XX 16-MAY-2002; 2002US-0380958P.  
XX  
XX (NISH/) NISHIMOTO I.  
PA  
XX Nishimoto I;  
PI  
XX WPI; 2004-061983/06.  
DR  
XX New Humanin derivative that protects a neuronal cell from cytotoxicity,  
PT useful for treating neurodegenerative disorders (e.g. Alzheimer's  
PT disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated  
PT amino acid.  
XX  
XX Example 1; SEQ ID NO 5; 82pp; English.  
PS  
XX The invention relates to a derivative of humanin (HN) that protects a  
CC neuronal cell from cytotoxicity, where the derivative contains at least  
CC one D-amino acid or phosphorylated amino acid, or where the derivative  
CC has an addition of one or more amino acids having an activity of forming  
CC a multimer. The humanin derivatives are useful in protecting neuronal  
CC cells from cytotoxicity related to neurodegenerative diseases. The  
CC composition and method are useful in treating neurodegenerative  
CC disorders, such as Alzheimer's disease. The present sequence represents a  
CC HN peptide derivative.  
CC  
XX  
XX Sequence 24 AA;  
SQ  
Query Match 100.0%; Score 120; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MAPRGFSCLLLTSEIDLPIVKRRA 24  
1 MAPRGFSCLLLTSEIDLPIVKRRA 24  
DB  
RESULT 14  
ADP95078  
ID ADP95078 standard; peptide; 24 AA.  
XX  
XX ADF95078;  
AC  
XX 26-FEB-2004 (first entry)  
DT  
XX  
XX Humanin (HN) wild-type peptide sequence.  
DE  
XX HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;  
KM Alzheimer's disease.  
KM  
XX Homo sapiens.  
OS  
XX WO2003097687-A2.  
PN  
XX 27-NOV-2003.  
PD  
XX 16-MAY-2003; 2003WO-JP006139.  
PF  
XX 16-MAY-2002; 2002US-0380958P.  
PR  
XX (NISH/) NISHIMOTO I.  
PA  
XX Nishimoto I;  
PI  
XX WPI; 2004-061983/06.  
DR  
XX N-PSDB; ADF95077.  
XX  
XX New Humanin derivative that protects a neuronal cell from cytotoxicity,  
PT useful for treating neurodegenerative disorders (e.g. Alzheimer's  
PT disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated  
PT amino acid.  
XX

PS Example; SEQ ID NO 27; 82pp; English.  
XX  
XX The invention relates to a derivative of humanin (HN) that protects a  
CC neuronal cell from cytotoxicity, where the derivative contains at least  
CC one D-amino acid or phosphorylated amino acid, or where the derivative  
CC has an addition of one or more amino acids having an activity of forming  
CC a multimer. The humanin derivatives are useful in protecting neuronal  
CC cells from cytotoxicity related to neurodegenerative diseases. The  
CC composition and method are useful in treating neurodegenerative  
CC disorders, such as Alzheimer's disease. The present sequence represents a  
CC HN wild-type peptide sequence.  
CC  
XX  
XX Sequence 24 AA;  
SQ  
Query Match 100.0%; Score 120; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MAPRGFSCLLLTSEIDLPIVKRRA 24  
1 MAPRGFSCLLLTSEIDLPIVKRRA 24  
DB  
RESULT 15  
ADP95058  
ID ADP95058 standard; peptide; 24 AA.  
XX  
XX ADF95058;  
AC  
XX 26-FEB-2004 (first entry)  
DT  
XX  
XX Humanin peptide derivative D-Ser14 HN.  
DE  
XX HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;  
KM Alzheimer's disease.  
KM  
XX Synthetic.  
OS  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH Misc-difference 14 /note="D-form residue"  
FT  
XX  
XX WO2003097687-A2.  
PN  
XX 27-NOV-2003.  
PD  
XX 16-MAY-2003; 2003WO-JP006139.  
PF  
XX 16-MAY-2002; 2002US-0380958P.  
PR  
XX (NISH/) NISHIMOTO I.  
PA  
XX Nishimoto I;  
PI  
XX WPI; 2004-061983/06.  
DR  
XX New Humanin derivative that protects a neuronal cell from cytotoxicity,  
PT useful for treating neurodegenerative disorders (e.g. Alzheimer's  
PT disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated  
PT amino acid.  
XX  
XX Claim 8; SEQ ID NO 7; 82pp; English.  
PS  
XX The invention relates to a derivative of humanin (HN) that protects a  
CC neuronal cell from cytotoxicity, where the derivative contains at least  
CC one D-amino acid or phosphorylated amino acid, or where the derivative  
CC has an addition of one or more amino acids having an activity of forming  
CC a multimer. The humanin derivatives are useful in protecting neuronal  
CC cells from cytotoxicity related to neurodegenerative diseases. The  
CC composition and method are useful in treating neurodegenerative  
CC disorders, such as Alzheimer's disease. The present sequence represents a  
CC HN peptide derivative.  
CC

XX Sequence 24 AA;

Query Match 100.0%; Score 120; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPRGFSCLLLTSEIDLPVKRRA 24  
|||  
Db 1 MAPRGFSCLLLTSEIDLPVKRRA 24

Search completed: March 28, 2006, 13:14:58  
Job time : 18.78 secs



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\* OM protein - protein search, using sw model

Run on: March 28, 2006, 13:15:18 ; Search time 3.136 Seconds  
(without alignments)  
736.353 Million cell updates/sec

Title: US-10-517-956-3  
Perfect score: 120  
Sequence: 1 MAPRGFSCLLLTSEIDLPIVKRRA 24

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	40.8	269	2	nitroreductase fam
2	46	38.3	359	2	transcription regu
3	45	37.5	220	2	hypothetical prote
4	44	36.7	90	2	prxs protein - Bnc
5	44	36.7	90	2	probable pheromone
6	44	36.7	92	1	QOBCXP
7	44	36.7	107	2	hypothetical prote
8	44	36.7	610	2	hypothetical prote
9	44	36.7	1796	2	serine/threonine k
10	43.5	36.2	319	2	B42891
11	43.5	36.2	1854	2	hypothetical prote
12	43	35.8	170	2	H71063
13	43	35.8	359	2	hypothetical prote
14	43	35.8	540	2	probable phosphat
15	43	35.8	570	2	membrane associat
16	42	35.0	143	1	heat shock protein
17	42	35.0	207	2	hypothetical prote
18	42	35.0	262	1	indole-3-glycerol-
19	42	35.0	381	2	probable bacterio
20	42	35.0	605	2	hypothetical prote
21	42	35.0	732	2	hypothetical prote
22	42	35.0	1584	2	protein P12M16.25
23	41.5	34.6	197	2	A70750
24	41	34.2	62	2	G82794
25	41	34.2	216	2	hypothetical prote
26	41	34.2	235	2	hypothetical prote
27	41	34.2	259	2	DNA-binding respon
28	41	34.2	264	2	conserved hypotet
29	41	34.2	378	2	probable malic enz

30	41	34.2	455	2	T09666	probable anthranil
31	41	34.2	543	2	AB0850	tyrosine phosphata
32	41	34.2	582	2	T15563	hypothetical prote
33	41	34.2	612	2	F96528	protein P27015.4
34	41	34.2	732	2	T31629	hypothetical prote
35	41	34.2	1227	2	T48028	hypothetical prote
36	41	34.2	2052	2	C97038	phage-related prot
37	41	34.2	4196	2	T43274	dynein heavy chain
38	40.5	33.8	586	2	E87363	sensor histidine k
39	40.5	33.8	610	2	A85870	probable transport
40	40.5	33.8	610	2	H91025	probable transport
41	40.5	33.8	610	2	B65001	probable transport
42	40.5	33.8	723	2	T32136	hypothetical prote
43	40	33.3	159	2	T30409	hypothetical prote
44	40	33.3	159	2	A97836	hypothetical prote
45	40	33.3	176	2	E90160	conserved hypotet

ALIGNMENTS

RESULT 1  
F97327  
nitroreductase family protein fused to ferredoxin domain [imported] - Clostridium acetob  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: F97327  
R:Noiling, J.; Bretton, G.; Ometchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: F97327  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-269 <KUR>  
A:Cross-references: UNIPROT:Q97D34; UNIPARC:UPI00000CA846; GB:AE001437; P1DN:AAK81409.1;  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC3483

Query Match 40.8%; Score 49; DB 2; Length 269;  
Best Local Similarity 50.0%; Pred. No. 3;  
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
DB 171 RGAPCLVLTADVDVP 186

RESULT 2  
AF3470  
transcription regulator [imported] - Brucella melitensis (strain 16M)  
C:Species: Brucella melitensis  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
R:DelVecchio, V.G.; Kapral, R.J.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I  
; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Levesc  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi  
A:Reference number: AD3252; PMID:11756688  
A:Accession: AF3470  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-359 <KUR>  
A:Cross-references: UNIPROT:Q8YEX3; UNIPARC:UPI00000581B8; GB:AE008917; P1DN:AAJ52929.1;  
C:Genetics:  
A:Gene: BMEL1748  
A:Map position: I  
Query Match 38.3%; Score 46; DB 2; Length 359;  
Best Local Similarity 43.5%; Pred. No. 12;

J. Bacteriol. 173, 7650-7664, 1991

QY 3 PRGFSCLLLTSEIDL PVK 21

J. Bacteriol. 173, 7650-7664, 1991

Db 86 PRGCCFWRLKREINCPFR 104

## RESULT 8

S76234

\*hypothetical protein - *Synechocystis* sp. (strain PCC 6803)

C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C:Accession: S76234

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 105-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76234

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-610 &lt;KAN&gt;

A:Cross-references: UNIPROT:P74396; UNIPARC:UPI0000000E76; EMBL:D90914; GB:AB001339; NID A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

## Query Match

Best Local Similarity 36.7%; Score 44; DB 2; Length 610;

Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 5 GPGSCLLLTSEIDLPVK 21

Db 18 GPGSCLEVLTLVMTGLK 34

## RESULT 9

AC1895

serine/threonine kinase with two-component sensor domain alr0709 [imported] - *Neotoc* sp.

C:Species: *Neotoc* sp. PCC 7120A:Note: *Neotoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C:Accession: AC1895

R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iritaghi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AC1895

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1796 &lt;KUR&gt;

A:Cross-references: UNIPROT:O8VYV3; UNIPARC:UPI000000CDE38; GB:BA000019; PIDN:BA072666.1; A:Experimental source: strain PCC 7120

C:Genetics: A:Gene: alr0709

## Query Match

Best Local Similarity 36.7%; Score 44; DB 2; Length 1796;

Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Oy 4 RGFSCLLLTSEIDLPVK 21

Db 862 KALSCLENDLSEIDLPVK 879

## RESULT 10

B42891

beta-galactosidase (BC 3.2.1.23), 36K chain - *Leuconostoc lactis* (strain NZ6009) plasmid

C:Species: *Leuconostoc lactis*

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C:Accession: B42891

R:David, S.; Stevens, H.; van Riel, M.; Simons, G.; de Vos, W.M. J. Bacteriol. 174, 4475-4481, 1992

A:Title: *Leuconostoc lactis* beta-galactosidase is encoded by two overlapping genes.

A:Reference number: A42891; MUID:92325034; PMID:1624440

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-319 <DAV>  
A:Cross-references: UNIPROT:Q02604; UNIPARC:UPI00001268F5; GB:M92281; NID:g149634; PIDN: C:Keywords: glycosidase; hydrolase

Query Match Best Local Similarity 36.2%; Score 43.5; DB 2; Length 319;

Matches 11; Conservative 4; Mismatches 7; Indels 7; Gaps 1;

Oy 2 APRGSCLLLTSEI-----DLPVKR 23

Db 249 APFAFSCPYPYAELENATNTEMLPLAR 277

## RESULT 11

T13576

hypothetical protein 52C10.5 - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004

C:Accession: T13576

R:Benos, P. submitted to the EMBL Data Library, February 1999

A:Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.

A:Reference number: 217690

A:Accession: T13576

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1854 &lt;SEN&gt;

A:Cross-references: UNIPROT:O96838; UNIPARC:UPI000008354E; EMBL:AL035311; NID:e1373062; A:introns: 4/3; 53/3; 209/3; 962/1; 1632/1; 1686/2; 1739/1; 1793/1

A:Note: EG:52C10.5

## Query Match

Best Local Similarity 36.2%; Score 43.5; DB 2; Length 1854;

Matches 12; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

Oy 3 PRGSCLLLTSEIDLPVKRRA 24

Db 714 PRGYTLRGSGSNELTRVRVA 736

## RESULT 12

H71063

hypothetical protein PH1206 - *Pyrococcus horikoshii*

C:Species: *Pyrococcus horikoshii*

C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatake, Y.; Hino, Y.; Yamamoto, S.; Sekine M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kuehda, N.; Oguchi, DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic ar

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: H71063

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-170 <KAW>  
A:Cross-references: UNIPROT:O58978; UNIPARC:UPI0000063002; GB:AP000005; NID:g3236132; PIR

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics: A:Gene: PH1206

## Query Match

Best Local Similarity 35.8%; Score 43; DB 2; Length 170;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 12 LTSEIDLPVKR 23

Db 103 LSSNIDIPVKR 114



GenCore version 5.1.7  
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\*OM protein - protein search, using sw model

Run on: March 28, 2006, 13:10:33 ; Search time 19.008 Seconds  
(without alignments)  
890.819 Million cell updates/sec

Title: US-10-517-956-3  
Perfect score: 120  
Sequence: 1 MAPRGFSCLLLTSEIDLPRKRA 24

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	24	1 HUNIN HUMAN	Q81v9g homo sapien
2	49	40.8	269	2 Q81D14 CLOAB	Q81D14 clostridium
3	49	40.8	1181	2 Q55X85 CRYNE	Q55X85 cryptococcu
4	49	40.8	1181	2 Q5KMP8 CRYNE	Q5KMP8 cryptococcu
5	48	40.0	208	2 Q6FTB3 AZOCA	Q6FTB3 azorhizobiu
6	48	40.0	223	2 Q8FMY2 COREF	Q8FMY2 corethobacte
7	48	40.0	427	1 DPF3 CHICK	P58270 gallus galli
8	48	40.0	542	2 Q5R9C4 PONPY	Q5R9C4 pongo pygma
9	47.5	39.6	527	2 Q89E87 BRAJA	Q89E87 bradyrhizob
10	47	39.2	387	2 Q5BA28 EMENT	Q5BA28 aspergillus
11	47	39.2	532	2 Q4MML4 SWICC	Q4MML4 arthrobacte
12	47	39.2	2404	2 Q6LPT6 PLAF7	Q6LPT6 plasmodium
13	46	38.3	163	2 Q59U23 CANAL	Q59U23 candida alb
14	46	38.3	106	2 Q86126 BRAJA	Q86126 bradyrhizob
15	46	38.3	322	2 Q5TFH7 BRUAB	Q5TFH7 bruceella ab
16	46	38.3	359	2 Q8YEX3 BRUME	Q8YEX3 bruceella me
17	46	38.3	359	2 Q424Y3 PLABE	Q424Y3 plasmodium
18	46	38.3	551	2 Q98N27 RHILLO	Q98N27 rhizobium 1
19	46	38.3	1412	2 Q7RGZ8 PLAYO	Q7RGZ8 plasmodium
20	45.5	37.9	412	2 Q9CU83 MOUSE	Q9CU83 mus musculu
21	45.5	37.9	490	1 FCXN3 HUMAN	FCXN3 homo sapien
22	45	37.5	50	2 Q64B16 9ARCH	Q64B16 uncultured
23	45	37.5	106	2 Q59V29 CANAL	Q59V29 candida alb
24	45	37.5	111	2 Q82T01 PYRAB	Q82T01 pyrobaculum
25	45	37.5	220	2 Q9YFG0 ASRBP	Q9YFG0 aeropyrum p
26	45	37.5	322	2 Q5YTB4 GRYPY	Q5YTB4 trypanosoma
27	45	37.5	326	2 Q54Q18 DICDI	Q54Q18 dictyosteli
28	45	37.5	452	2 Q943G2 ORISA	Q943G2 oryza sativ
29	45	37.5	403	2 Q59UP4 CANAL	Q59UP4 candida alb
30	45	37.5	652	2 Q7QPV8 GIALA	Q7QPV8 gliardia lam
31	45	37.5	783	2 Q7S0E8 NEUCR	Q7S0E8 neurospora

32	45	37.5	1110	2 Q4WD02 ASPRU	Q4WD02 aspergillus
33	45	37.5	1273	2 Q4WR26 ASPFU	Q4WR26 aspergillus
34	45	37.5	1751	2 Q4WAX7 ASPFU	Q4WAX7 aspergillus
35	45	37.5	1751	2 Q4WB48 ASPFU	Q4WB48 aspergillus
36	45	37.5	1761	2 Q4WB22 ASPFU	Q4WB22 aspergillus
37	45	37.5	2954	2 Q4IRV3 GIBZE	Q4IRV3 gibberella
38	44.5	37.1	120	2 Q9PT93 BRARE	Q9PT93 brachydanio
39	44.5	37.1	263	2 Q5TYT5 BRARE	Q5TYT5 brachydanio
40	44.5	37.1	922	2 Q4WXJ9 ASPFU	Q4WXJ9 aspergillus
41	44.5	37.1	1691	2 Q9GRE7 LEIMA	Q9GRE7 leishmania
42	44	36.7	89	2 Q5BR02 SCHUA	Q5BR02 schistosoma
43	44	36.7	90	2 Q5G3Q4 ENTFA	Q5G3Q4 enterococcu
44	44	36.7	98	2 P77203 ECOLI	P77203 escherichia
45	44	36.7	107	2 Q9PLR9 CHLMU	Q9PLR9 chlamydia m

## ALIGNMENTS

RESULT 1	HUNIN HUMAN	STANDARD;	PRT;	24 AA.
ID	HUNIN HUMAN			
AC	Q81V9G			
DT	25-OCT-2004 (Rel. 45, Created)			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Humanin.			
CN	Name=HN;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE			
RP	SPECIFICITY.			
RC	TISSUE=Brain;			
RX	MEDLINE=21265469; PubMed=11371646; DOI=10.1073/pnas.101133498;			
RA	Hashimoto Y., Nikiura T., Tajima H., Yasukawa T., Sudo H., Ito Y.,			
RA	Kita Y., Kawasumi M., Kouyama K., Doym M., Sobue G., Koide T.,			
RA	Tsuji S., Tang J., Kurokawa K., Hashimoto I.,			
RT	"A rescue factor abolishing neuronal cell death by a wide spectrum of			
RT	familial Alzheimer's disease genes and Abeta.",			
RT	Proc. Natl. Acad. Sci. U.S.A. 98:6336-6341(2001).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE, AND INTERACTION WITH IGFBP3.			
RX	PubMed=14561895; DOI=10.1073/pnas.2135111100;			
RA	Ikonen M., Liu B., Hashimoto Y., Ma L., Lee K.W., Nikiura T.,			
RA	Nishimoto I., Cohen P.,			
RT	"Interaction between the Alzheimer's survival peptide humanin and			
RT	insulin-like growth factor-binding protein 3 regulates cell survival			
RT	and apoptosis.",			
RT	Proc. Natl. Acad. Sci. U.S.A. 100:13042-13047(2003).			
RN	[3]			
RP	EVIDENCE OF IN VIVO EXPRESSION, AND TISSUE SPECIFICITY.			
RC	TISSUE=Brain;			
RX	MEDLINE=22007889; PubMed=12009529; DOI=10.1016/S0304-3940(02)00199-4;			
RA	Tajima H., Nikiura T., Hashimoto Y., Ito Y., Kita Y., Terashita K.,			
RA	Yamazaki K., Koto A., Aiso S., Nishimoto I.,			
RT	"Evidence for in vivo production of Humanin peptide, a neuroprotective			
RT	factor against Alzheimer's disease-related insults.",			
RT	Neurosci. Lett. 324:227-231(2002).			
RL	[4]			
RP	FUNCTION, AND MUTAGENESIS OF 1-MET--ALA-2; 1-MET--PRO-3; CYS-8;			
RP	SER-14; 19-PRO--ALA-24 AND 20-VAL--ALA-24.			
RX	PubMed=1171757;			
RA	Hashimoto Y., Nikiura T., Ito Y., Sudo H., Hata M., Arakawa E.,			
RA	Abe Y., Kita Y., Nishimoto I.,			
RT	"Detailed characterization of neuroprotection by a rescue factor			
RT	humanin against various Alzheimer's disease-relevant insults.",			
RT	J. Neurosci. 21:9235-9245(2001).			
RN	[5]			
RP	INTERACTION WITH BAX.			

RX PubMed:12732850; DOI=10.1038/nature01627;  
 RA Guo B., Zhai D., Cabezas E., Welsh K., Nouraini S., Satterthwaite A.C.,  
 RA Reed J.C.;  
 RT "Humanin peptide suppresses apoptosis by interfering with Bax  
 RT activation.";  
 RL Nature 423:456-461(2003).  
 RN [6].  
 RP INTERACTION WITH TRIM11.  
 RX PubMed:12670303; DOI=10.1046/j.1460-9568.2003.02553.x;  
 RA Nakura T., Hashimoto Y., Tajima H., Ishizaka M., Yamagishi Y.,  
 RA Kawasumi M., Nawa M., Terashita K., Aiso S., Nishimoto I.;  
 RT "A tripartite motif protein TRIM1 binds and destabilizes Humanin, a  
 RT neuroprotective peptide against Alzheimer's disease-relevant  
 RT insults.";  
 RL Eur. J. Neurosci. 17:1150-1158(2003).  
 RN [7].  
 RP FUNCTION.  
 RX PubMed:15153530;  
 RA Ying G., Iribarren P., Zhou Y., Gong W., Zhang N., Yu Z.-X., Le Y.,  
 RA Cui Y., Wang J.M.;  
 RT "Humanin, a newly identified neuroprotective factor, uses the G  
 RT protein-coupled formylpeptide receptor-like-1 as a functional  
 RT receptor.";  
 RL J. Immunol. 172:7078-7085(2004).  
 CC -1- FUNCTION: Plays a role as a neuroprotective factor against death  
 CC induced by multiple different types of familial Alzheimer's  
 CC disease genes and beta amyloid in Alzheimer disease. Induced  
 CC chemotaxis of mononuclear phagocytes by using FPR1. Reduced the  
 CC aggregation and fibrillary formation by suppressing the effect of  
 CC APP on mononuclear phagocytes and acts by competitively inhibiting  
 CC the access of FPR1 to APP. Prevents the translocation of BAX from  
 CC cytosol to mitochondria.  
 CC -1- SUBUNIT: Interacts with IGFBR3, BAX and TRIM1.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed in the heart, skeletal muscles,  
 CC kidney and liver. Lesser but significant expression is observed in  
 CC the brain and the gastrointestinal tract. Expressed in the AD  
 CC brain, where it is found in some of the large intact neurons of  
 CC the occipital lobes and small and round reactive glial cells in  
 CC the hippocampus.  
 CC -1- INDUCTION: Release is regulated by intracellular mechanism. The  
 CC intracellular level is regulated by TRIM1 through the proteasomal  
 CC pathway.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; AY029066; AAK50430.1; -; mRNA.  
 DR MM; 606120; -;  
 FT REGION 3 19 Responsible for the neuroprotective  
 FT COMPBIAS 9 12 activity.  
 FT MUTAGEN 1 3 Poly-Leu.  
 FT MUTAGEN 1 2 Missing: Abolishes the neuroprotective  
 FT MUTAGEN 1 2 activity.  
 FT MUTAGEN 8 8 Missing: No effect on the neuroprotective  
 FT MUTAGEN 8 8 activity.  
 FT MUTAGEN 8 8 C->A,D,E,F,G,I,L,M,N,P,Q,S,T,V,W,Y;  
 FT MUTAGEN 8 8 Abolishes the neuroprotective activity.  
 FT MUTAGEN 8 8 C->H: Significantly reduces the  
 FT MUTAGEN 8 8 neuroprotective activity.  
 FT MUTAGEN 8 8 C->K,R: No effect on the neuroprotective  
 FT MUTAGEN 14 14 activity.  
 FT MUTAGEN 14 14 S->A: Abolishes the neuroprotective  
 FT MUTAGEN 14 14 activity.  
 FT MUTAGEN 14 14 S->G: Potentiation of the neuroprotective  
 FT MUTAGEN 19 24 activity.  
 FT MUTAGEN 20 24 Missing: Abolishes the neuroprotective  
 FT activity.  
 FT Missing: No effect on the neuroprotective  
 FT activity.

SEQ SEQUENCE 24 AA; 2687 MW; 08B9A778EC13B971 CRC64;  
 Query Match 100.0%; Score 120; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 4, 9e-12;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPRGFSCILLTSEIDLPVKRRA 24  
 DB 1 MAPRGFSCILLTSEIDLPVKRRA 24  
 RESULT 2  
 Q97DU4\_CLOAB  
 ID Q97DU4\_CLOAB PRELIMINARY; PRT; 269 AA.  
 AC Q97DU4;  
 DT 01-OCT-2001 (TREMBLrel. 18, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Nitroreductase family protein fused to ferredoxin domain.  
 GN OideredLocuNames=CAC3483;  
 OS Clostridium acetobutylicum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 CX NCBI\_TaxID=1488;  
 RN [1].  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE=21359325; PubMed=1466286;  
 RX DOI=10.1128/JB.183.16.4823-4838.2001;  
 RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,  
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,  
 RA Tatusov R.L., Sabathe P., Doucette-Stamm L.A., Soucaille P.,  
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;  
 RT "Genome sequence and comparative analysis of the solvent-producing  
 RT bacterium Clostridium acetobutylicum.";  
 RL J. Bacteriol. 183:4823-4838(2001).  
 DR EMBL; AB007845; AAK81409.1; -; Genomic\_DNA.  
 DR FTR; F97327; F97327.  
 DR HSP; P00193; 1DUR.  
 DR GO; GO:0005489; F:electron transporter activity; IEA.  
 DR GO; GO:0005506; F:iron ion binding; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; F:electron transport; IEA.  
 DR InterPro; IPR001450; 4Fe4S\_Ferredoxin.  
 DR InterPro; IPR000415; Nitroreductase.  
 DR Pfam; PF00037; Fe4; 2.  
 DR Pfam; PF00881; Nitroreductase; 1.  
 DR PRINTS; PR00353; 4FE4SFDOXIN.  
 DR PROSITE; PS00198; 4FE4S\_FERRDOXIN; 2.  
 KW Complete proteome.  
 SQ SEQUENCE 269 AA; 30163 MW; BFE8734FBA3E951 CRC64;  
 Query Match 40.8%; Score 49; DB 2; Length 269;  
 Best Local Similarity 50.0%; Pred. No. 24;  
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 4 RGFSCLLLTSEIDLP 19  
 DB 171 RGAPCLVATADVDFP 166  
 RESULT 3  
 Q55X85\_CRYNE  
 ID Q55X85\_CRYNE PRELIMINARY; PRT; 1181 AA.  
 AC Q55X85;  
 DT 13-SEP-2005 (TREMBLrel. 31, Created)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=CNBB4770;  
 OS Cryptococcus neoformans var. neoformans B-3501A.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 OC Tremellomycetiales; Tremellales; Tremellaceae; Filobasidiella.

```

OK NCB1_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
  Wicker B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
  preliminary data.
DR EMBL; AAEY0100011; EAL22302.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1181 AA; 130133 MW; 825BF00F2CDD4C00 CRC64;

Query Match 40.8%; Score 49; DB 2; Length 1181;
Best Local Similarity 41.7%; Pred. No. 1.1e+02;
Matches 10; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MAPRGSCLLLTSEIDLPIVKRRA 24
Db 379 LRPRALTCLLLSQDTPDPVPRHDA 402

RESULT 4
Q5KMP8 CRYNE PRELIMINARY; PRT; 1181 AA.
ID Q5KMP8;
AC Q5KMP8;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CNB00940;
OS Cryptococcus neoformans var. neoformans JEC21.
OC Bakaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCB1_TaxID=214684;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JEC21;
RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Uterback T.,
  Van Aalen S., Fraser C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JEC21;
RA Donlin M.;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=JEC21;
RX PubMed=15653466; DOI=10.1126/science.1103773;
RA Lotfian B.-J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
  Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
  Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
  D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
  Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywnicki M.I.,
  Kwon-Chung K.J., Lengele K.B., Maiti R., Marra M.A., Marra R.E.,
  Mathewson C.A., Mitchell T.G., Petrea M., Riggs F.R., Salzberg S.L.,
  Schein J.E., Shvartsbeyn A., Shin H., Shumway L., Specht C.A.,
  Suh B.B., Tenney A., Uterback T.R., Wicker B.L., Mortman J.R.,
  Wye N.H., Kronstad J.W., Lodge J.K., Heltman J., Davis R.W.,
  Fraser C.M., Hyman R.W.;
RT "The genome of the basidiomycetous yeast and human pathogen
  Cryptococcus neoformans.";
RL Science 307:1321-1324(2005).
DR EMBL; AB017342; AA041793.1; -; Genomic_DNA.
DR InterPro; IPR011989; ARM-1like.
DR Pfam; PF02985; HEAT_2.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1181 AA; 130134 MW; 825BF00F2CDD4C00 CRC64;

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Query Match 40.8%; Score 49; DB 2; Length 1181;
Best Local Similarity 41.7%; Pred. No. 1.1e+02;
Matches 10; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MAPRGSCLLLTSEIDLPIVKRRA 24
Db 379 LRPRALTCLLLSQDTPDPVPRHDA 402

RESULT 5
Q6PTB3 AZOCA
ID Q6PTB3;
AC Q6PTB3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE hnpd.
GN Name=hnpd;
OS Azorhizobium caulinodans.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Azorhizobium.
OX NCB1_TaxID=7;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ORS571;
RX MEDLINE=2235395; PubMed=12324339;
RX DOI=10.1128/AEM.68.10.4915-4924.2002;
RA Baginsky C., Brito B., Imperial J., Palacios J.M., Ruiz-Argueso T.;
RT "Diversity and evolution of hydrogenase systems in rhizobia.";
RL Appl. Environ. Microbiol. 68:4915-4924(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ORS571;
RX PubMed=15321689; DOI=10.1016/j.fems.2004.07.003;
RA Baginsky C., Palacios J.M., Imperial J., Ruiz-Argueso T., Brito B.;
RT "Molecular and functional characterization of the Azorhizobium
  caulinodans ORS571 hydrogenase gene cluster.";
RL FEMS Microbiol. Lett. 237:399-405(2004).
RN EMBL; AY581127; AAS91029.1; -; Genomic_DNA.
DR GO; GO:0009375; C:ferredoxin hydrogenase complex; IEA.
DR GO; GO:0008901; F:ferredoxin hydrogenase activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004222; F:metallopeptidase activity; IEA.
DR GO; GO:0016485; P:protein processing; IEA.
DR InterPro; IPR006671; Peptidase M52.
DR InterPro; IPR004419; Pept_M52_HyD.
DR InterPro; IPR006227; Pept_M52_mat.
DR Pfam; PF01750; Hycl_1.
DR PRINTS; PR00446; HYDRGNUPRAK.
DR TIGRFAMs; TIGR00140; hnpd.fhnd.pepf.1.
DR TIGRFAMs; TIGR00141; hnpd.fhnd.pepf.1.
DR TIGRFAMs; TIGR00072; hnpd.fhnd.pepf.1.
SQ SEQUENCE 208 AA; 22061 MW; 75C7B4B280B3724 CRC64;

Query Match 40.8%; Score 48; DB 2; Length 208;
Best Local Similarity 47.8%; Pred. No. 27;
Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MAPRGSCLLLTSEIDLPIVKRRA 23
Db 142 VAAVAVTEVALLTSEIDPVPVPR 164

RESULT 6
Q8FMY9 COREF
ID Q8FMY9;
AC Q8FMY9;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Putative carboxylase.
GN OrderedLocNames=CB2360;
OS Corynebacterium efficiens.

```





RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR859465; CAH91636.1; -; mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0015075; F:ion transporter activity; IEA.  
 DR GO; GO:0015293; F:symporter activity; IEA.  
 DR GO; GO:0006811; P:ion transport; IEA.  
 DR GO; GO:0006814; P:sodium ion transport; IEA.  
 DR InterPro; IPR007114; MFS.  
 DR InterPro; IPR011701; MFS\_1.  
 DR InterPro; IPR004749; Orgcat\_transp.  
 DR InterPro; IPR005829; Sug\_transporter.  
 DR Pfam; PF07690; MFS\_1; 1.  
 DR TIGRFAMs; TIGR00898; 2A0119; 1.  
 DR PROSITE; PS00850; MFS; 1.  
 DR PROSITE; PS00216; SUGAR\_TRANSPORT\_1; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 542 AA; 59847 MW; PAF2E14949E711B0 CRC64;

Query Match 40.0%; Score 48; DB 2; Length 542;  
 Best Local Similarity 64.3%; Pred. No. 71;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 PRGSCULLLT---SEIDLPVKRRA 24  
 Db 423 PSFSCFLFYLTSEL 436

RESULT 9  
 Q89887\_BRAJA PRELIMINARY; PRT; 527 AA.  
 ID Q89887\_BRAJA  
 AC Q89887;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE B117200 protein.  
 GN OrderedLocusNames=B117200;  
 OS Bradyrhizobium japonicum.  
 OC Bradyrhizobium japonicum.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae; Bradyrhizobiium.  
 OC NCBI\_TaxID=375;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=USDA 110;  
 RX MEDLINE=22484998; PubMed=12597275;  
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,  
 RA Sasamoto S., Watanabe A., Idegawa K., Iritschi M., Kawashima K.,  
 RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,  
 RA Tabata S.;  
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
 RT Bradyrhizobium japonicum USDA110.";  
 RT DNA Res. 9:189-197(2002).  
 RL EMBL; BA000040; BAC52465.1; -; Genomic DNA.  
 DR GO; GO:0005215; F:transporter activity; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR000914; SBP\_bac\_5.  
 DR InterPro; IPR006311; Tat.  
 DR InterPro; IPR001680; WD40.  
 DR Pfam; PF00496; SBP\_bac\_5; 1.  
 DR TIGRFAMs; TIGR01409; TAT\_signal\_seq; 1.  
 DR PROSITE; PS00678; WD\_REPEATS\_1; UNKNOWN\_1.  
 KW Complete proteome.  
 SQ SEQUENCE 527 AA; 57740 MW; 7ECBE1BB1C0FCS CRC64;

Query Match 39.6%; Score 47.5; DB 2; Length 527;  
 Best Local Similarity 44.0%; Pred. No. 84;  
 Matches 11; Conservative 3; Mismatches 8; Indels 3; Gaps 1;

Qy 3 PRGSCULLLT---SEIDLPVKRRA 24  
 Db 281 PRGYACMLRLNHLQPPFDPNPAVRRA 305

RESULT 10  
 Q5BA28\_EMENI PRELIMINARY; PRT; 387 AA.  
 ID Q5BA28\_EMENI  
 AC Q5BA28;  
 DT 10-MAY-2005 (TREMBLrel. 30, Created)  
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=AN2602.2;  
 OS Aspergillus nidulans FGSC A4.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eukaryotes; Trichocomaceae; Emericella.  
 OC NCBI\_TaxID=227321;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FGSC A4;  
 RA Birren B., Nussbaum C., Abouelleil A., Allen N., Anderson S.,  
 RA Archchil H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,  
 RA Boukhgalter B., Butler J., Calvo S.B., Camarata J., Chang J.,  
 RA Chepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,  
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,  
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,  
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hefez N.,  
 RA Hagopian D., Hagos B., Hall J., Horton L., Huime W., Iliev I.,  
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,  
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,  
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald J., Major J., Manning J.,  
 RA Matthews C., Mauceli E., McCarthy M., Meldrum J., Menes L.,  
 RA Minova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,  
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,  
 RA Oliver J., Peterson K., Pihunkhang P., Pierre N., Purcell S.,  
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,  
 RA Roman J., Schauer S., Schupbach R., Seaman S., Severy C., Smirnov S.,  
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,  
 RA Talamas J., Tesfaye S., Theodore J., Tophan K., Travers M.,  
 RA Vasilleev H., Venkatarman V.S., Viel R., Vo A., Wang S., Wilson B.,  
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,  
 RA Lander B.;  
 RT "Genome Sequence of Aspergillus nidulans."  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AAC0100043; EAA64707.1; -; Genomic DNA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR InterPro; IPR000379; Ser\_estrs.  
 DR Hydrolase; Hypothetical protein.  
 SQ SEQUENCE 387 AA; 42761 MW; ACCJ134337251054 CRC64;

Query Match 39.2%; Score 47; DB 2; Length 387;  
 Best Local Similarity 75.0%; Pred. No. 74;  
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 13 TSEIDLPVKRRA 24  
 Db 60 TSEIQIPLKRRRA 71

RESULT 11  
 Q4NNM4\_9M1CC PRELIMINARY; PRT; 532 AA.  
 ID Q4NNM4\_9M1CC  
 AC Q4NNM4;  
 DT 13-SEP-2005 (TREMBLrel. 31, Created)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
 DE Similar to Sugar diacid utilization regulator.  
 GN ORFNames=ArthDRAPT\_3900;  
 OS Arthrobacter sp. FB24.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Micrococciaceae; Micrococciaceae; Arthrobacter.  
 OC NCBI\_TaxID=290399;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FB24;  
 RG US DOE Joint Genome Institute (JGI-PGF);

RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,  
RA Hammon N., Israeli S., Pitluck S., Richardson P.,  
RT "Sequencing of the draft genome assembly of *Archaeobacter* sp. FB24.";  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FB24;  
RG US DOE Joint Genome Institute (PGF-ORNL);  
RA Laximier F., Land M.;  
RT "Annotation of the draft genome assembly of *Archaeobacter* sp. FB24.";  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAG01000001; EAL98032.1; -; Genomic DNA.  
SQ SEQUENCE 532 AA; 57662 MW; 58148F8B1D07465F CRC64;

Query Match 39.2%; Score 47; DB 2; Length 532;  
Best Local Similarity 45.0%; Pred. No. 1e+02;  
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 3 PRGFCLLLTSEIDL PVK 22  
Db 14 PLGFASLLLRPSRADSPER 33

RESULT 12  
ID 06LF76\_PLAF7 PRELIMINARY; PRT; 2404 AA.  
AC 06LF76;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein (Protein kinase, putative).  
GN ORFNames=PF145C;  
OS Plasmodium falciparum (isolate 3n7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=36329;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=3D7;  
RX MEDLINE=2255708; PubMed=1236867; DOI=10.1038/nature01095;  
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,  
RA Mungall K., Bowman S., Atkin R., Baker S., Barton A., Brooks K.,  
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,  
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,  
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,  
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,  
RA Harper D., Hauber H., Hornby T., Holroyd S., Horrocks F.,  
RA Humphray S., Jagels K., James K.D., Johnson D., Kethornou A.,  
RA Knights A., Kontorov B., Kyes S., Larke N., Lawson D., Leonard N.,  
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,  
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,  
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,  
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,  
RA Taylor K., Thave A., Unwin L., Whitehead S., Woodward J.,  
RA Sultson J.E., Craig A., Newbold C., Barrell B.G.;  
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";  
RL Nature 419:527-531(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=3D7;  
RA Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K.,  
RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,  
RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.G.;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR382400; CAG25050.1; -; Genomic DNA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein tyrosine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_Thr\_kinase.

DR InterPro; IPR001245; Tyr\_kinase.  
DR Pfam; PF00659; Kinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00219; TyKc; 1.  
DR PROSITE; PSS0011; PROTEIN\_KINASE\_DOM; 1.  
KM Hypothetical protein, kinase.  
SQ SEQUENCE 2404 AA; 279784 MW; EB0162E3ABD024B4 CRC64;

Query Match 39.2%; Score 47; DB 2; Length 2404;  
Best Local Similarity 50.0%; Pred. No. 4.6e+02;  
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MAPRGSCLLLTSEIDL 18  
Db 2308 MAPETFSCTTEVTEKIDI 2325

RESULT 13  
ID 059U23\_CANAL PRELIMINARY; PRT; 106 AA.  
AC 059U23;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=Ca019.3748;  
OS Candida albicans SC5314.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=237561;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=SC5314;  
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;  
RA Jones T., Federapfel N.A., Chibana H., Dungan J., Kalman S.,  
RA Magee B.B., Newport G., Thortenson Y.R., Agabian N., Magee P.T.,  
RA Davis R.W., Scherer S.;  
RT "The diploid genome sequence of *Candida albicans*.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=SC5314;  
RA Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegbola O.,  
RA Roberts J., Persson K., Donnelly S., Favoretto S., Tsung K.-W.,  
RA Jones T., Scherer S., Agabian N.;  
RT "Annotation of the Genome of *Candida albicans*.";  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAC001000127; EAK94320.1; -; Genomic DNA.  
KM Hypothetical protein.  
SQ SEQUENCE 106 AA; 11772 MW; 33DF49BDCB1305C8 CRC64;

Query Match 38.3%; Score 46; DB 2; Length 106;  
Best Local Similarity 61.5%; Pred. No. 30;  
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 9 LLLTSEIDL PVK 21  
Db 70 LLLTTEIDQPIK 82

RESULT 14  
ID 086126\_BRAJA PRELIMINARY; PRT; 163 AA.  
AC 086126; Q79V08;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein (Bl10903 protein).  
GN OrderedLocNames=Bl10903;

Search completed: March 28, 2006, 13:20:02  
Job time : 21.008 secs

OS Bradyrhizobium japonicum.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae; Bradyrhizobium.  
OX NCBI\_TaxID=375;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=1108pc4;  
RX MEDLINE=98348447; PubMed=9683482;  
RA Bauer E., Kaspar T., Fischer H.M., Hennecke H.;  
"Expression of fixK<sub>hfa</sub> operon in Bradyrhizobium japonicum depends on  
a new response regulator system, RegR.";  
\*T J. Bacteriol. 180:3853-3863(1998).  
RL [2]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=USDA 110;  
RC MEDLINE=22484998; PubMed=12597275;  
RA Kaneko T., Nakamura Y., Sato S., Minamimawa K., Uchiumi T.,  
Sasanoto S., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,  
Tabata S.;  
"Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
Bradyrhizobium japonicum USDA110.";  
\*RL DNA Res. 9:189-197(2002).  
DR EMBL; AJ006100; CAA06860.1; -; Genomic DNA.  
DR EMBL; BA000040; BAC46168.1; -; Genomic DNA.  
DR InterPro; IPR009394; DUF1052.  
DR Pfam; PF06319; DUF1052; 1.  
KM Complete proteome; Hypothetical protein.  
SQ SEQUENCE 163 AA; 18262 MW; 192132E03DE83D6 CRC64;

Query Match 38.3%; Score 46; DB 2; Length 163;  
Best Local Similarity 55.0%; Pred. No. 45;  
Matches 11; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

OY 5 GFSCLLTSEIDLPVKRR 24  
DB 37 GFSCI---SELPLPSGRRA 52

RESULT 15  
O57FH7 BRUAB  
ID O57FH7\_BRUAB PRELIMINARY; PRT; 322 AA.  
AC O57FH7;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Transcriptional regulator, Pfs family.  
GN OrderedLocustNames=Brubd1\_0196;  
OS Brucella abortus.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=235;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=9-941 / Biovar 1;  
RX PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;  
RA Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuermer R.L.,  
Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;  
"Completion of the genome sequence of Brucella abortus and comparison  
to the highly similar genomes of Brucella melitensis and Brucella  
suis.";  
\*RT J. Bacteriol. 187:2715-2726(2005).  
RL EMBL; AE017223; AAX73607.1; -; Genomic DNA.  
KM Complete proteome.  
SQ SEQUENCE 322 AA; 34746 MW; 2C912CFPE235402A CRC64;

Query Match 38.3%; Score 46; DB 2; Length 322;  
Best Local Similarity 43.5%; Pred. No. 90;  
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

OY 1 MAPRGFSCLLTSEIDLPVKRR 23  
DB 79 MAVGVGVCVTLADNNGVPIERR 101

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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:20:18 / Search time 4.288 Seconds  
(without alignments)  
462.737 Million cell updates/sec

Title: US-10-517-956-3  
120  
Perfect score: 120  
Sequence: 1 MAPRGFSCLLLTSEIDLVPVKRRA 24

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents AA.\*  
2: /cgn2\_6/ptodata/1/1aa/5\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCrus\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	40.0	466	2	US-09-902-540-11091, A Sequence 11091, A
2	45	37.5	460	2	US-09-248-796A-16093, A Sequence 16093, A
3	43	35.8	145	2	US-09-252-991A-18594, A Sequence 18594, A
4	43	35.8	178	2	US-09-252-991A-17622, A Sequence 17622, A
5	43	35.8	537	1	US-08-647-197-2, A Sequence 2, Appli
6	43	35.8	597	2	US-09-252-991A-22560, A Sequence 22560, A
7	42	35.0	109	1	US-08-647-397-4, A Sequence 4, Appli
8	42	35.0	138	2	US-09-489-039A-11748, A Sequence 11748, A
9	42	35.0	542	2	US-09-614-891-10, A Sequence 10, Appli
10	41.5	34.6	338	2	US-09-902-540-15112, A Sequence 15112, A
11	41	34.2	113	2	US-09-489-039A-12316, A Sequence 12316, A
12	41	34.2	155	2	US-09-488-039A-9041, A Sequence 9041, Ap
13	41	34.2	228	2	US-09-182-145-19, A Sequence 19, Appli
14	41	34.2	229	2	US-09-182-145-99, A Sequence 99, Appli
15	41	34.2	230	2	US-09-182-145-98, A Sequence 98, Appli
16	41	34.2	231	2	US-09-182-145-97, A Sequence 97, Appli
17	41	34.2	232	2	US-09-182-145-96, A Sequence 96, Appli
18	41	34.2	233	2	US-09-182-145-95, A Sequence 95, Appli
19	41	34.2	234	2	US-09-182-145-94, A Sequence 94, Appli
20	41	34.2	235	2	US-09-182-145-93, A Sequence 93, Appli
21	41	34.2	236	2	US-09-182-145-92, A Sequence 92, Appli
22	41	34.2	237	2	US-09-182-145-91, A Sequence 91, Appli
23	41	34.2	238	2	US-09-182-145-90, A Sequence 90, Appli
24	41	34.2	239	2	US-09-182-145-89, A Sequence 89, Appli
25	41	34.2	240	2	US-09-182-145-88, A Sequence 88, Appli
26	41	34.2	241	2	US-09-182-145-87, A Sequence 87, Appli
27	41	34.2	242	2	US-09-182-145-86, A Sequence 86, Appli

28	41	34.2	243	2	US-09-182-145-85, A Sequence 85, Appli
29	41	34.2	244	2	US-09-182-145-84, A Sequence 84, Appli
30	41	34.2	245	2	US-09-182-145-83, A Sequence 83, Appli
31	41	34.2	246	2	US-09-182-145-82, A Sequence 82, Appli
32	41	34.2	247	2	US-09-182-145-81, A Sequence 81, Appli
33	41	34.2	248	2	US-09-182-145-80, A Sequence 80, Appli
34	41	34.2	249	2	US-09-182-145-79, A Sequence 79, Appli
35	41	34.2	250	2	US-09-182-145-78, A Sequence 78, Appli
36	41	34.2	251	2	US-09-182-145-77, A Sequence 77, Appli
37	41	34.2	252	2	US-09-252-991A-19237, A Sequence 19237, A
38	41	34.2	451	2	US-09-252-991A-31986, A Sequence 31986, A
39	41	34.2	452	2	US-09-457-046B-72, A Sequence 72, Appli
40	41	34.2	453	2	US-09-866-570B-72, A Sequence 72, Appli
41	41	34.2	495	2	US-09-252-991A-20739, A Sequence 20739, A
42	41	34.2	528	2	US-08-987-691A-4, A Sequence 4, Appli
43	41	34.2	563	2	US-08-987-691A-2, A Sequence 2, Appli
44	40.5	33.8	231	2	US-09-182-145A-207, A Sequence 207, Appli
45	40	33.3	25	1	US-07-966-187-4, A Sequence 4, Appli

#### ALIGNMENTS

```
RESULT 1
US-09-902-540-11091
; Sequence 11091, Application US/0902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11091
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; US-09-902-540-11091

Query Match      40.0%; Score 48; DB 2; Length 466;
Best Local Similarity 48.3%; Pred. No. 6.8;
Matches 14; Conservative 2; Mismatches 7; Indels 6; Gaps 1;

Oy      2  APRGFSCLLTSEIDLVPVKRRA 24
Db      411 APRGFSARGFGLLVPRDLYVYVMA 439

RESULT 2
US-09-248-796A-16093
; Sequence 16093, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Welstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16093
; LENGTH: 460
; TYPE: PRT
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; ORGANISM: Candida albicans
US-09-248-796A-16093
Query Match 37.5%; Score 45; DB 2; Length 460;
Best Local Similarity 47.4%; Pred. No. 22;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MAPRGFSCLLLTSEIDLP 19
Db 159 IAPRGNSCPICLTDDFVAP 177

RESULT 3
US-09-252-991A-18594
; Sequence 18594, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18594
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18594
Query Match 35.8%; Score 43; DB 2; Length 145;
Best Local Similarity 47.4%; Pred. No. 13;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 APRGFSCLLTSEIDLPV 20
Db 29 APRMACCCVMTAIIIRPM 47

RESULT 4
US-09-252-991A-17622
; Sequence 17622, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17622
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17622
Query Match 35.8%; Score 43; DB 2; Length 178;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LLTSEIDLPVKRR 23
Db 88 LVLRERLDLPVRRR 101
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RESULT 5
US-08-647-397-2
; Sequence 2, Application US/08647397
; Patent No. 5972702
; GENERAL INFORMATION:
; APPLICANT: Belter, David R.
; APPLICANT: Brady, Kevin P.
; TITLE OF INVENTION: OSTEOCLAST TRANSPORTER
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacke, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,397
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: B0801/7048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 537 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-647-397-2
Query Match 35.8%; Score 43; DB 1; Length 537;
Best Local Similarity 55.6%; Pred. No. 60;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 6 FSCLLLTSEIDLPVKRR 23
Db 426 FSCFLYTSSELYPTVLARQ 443

RESULT 6
US-09-252-991A-22560
; Sequence 22560, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22560
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22560
Query Match 35.8%; Score 43; DB 2; Length 597;
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Best Local Similarity 50.0%; Pred. No. 67;  
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
Qy 5 GFSCLLLTSEIDPVKRR 24  
Db 277 GFCACALLLALRLVLVKKRA 296

RESULT 7  
US-08-647-397-4

Sequence 4, Application US/08647397  
Patent No. 5972702  
GENERAL INFORMATION:  
APPLICANT: Beier, David R.  
APPLICANT: Brady, Kevin P.  
TITLE OF INVENTION: OSTEOCLAST TRANSPORTER  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/647,397  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Gates, Edward R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: B0801/7048  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-647-397-4

Query Match 35.0%; Score 42; DB 1; Length 109;  
Best Local Similarity 72.7%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FSCLLLTSEI 16  
Db 57 FSCFLYTSYL 67

## RESULT 8

US-09-489-039A-11748  
Sequence 11748, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLASSTELLA  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 11748  
LENGTH: 138  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-11748

Query Match 35.0%; Score 42; DB 2; Length 138;  
Best Local Similarity 46.7%; Pred. No. 18;  
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 9 LLTSEIDPVKRR 23  
Db 43 VIFVTSAYEYVKKR 57

## RESULT 9

US-09-614-891-10  
Sequence 10, Application US/09614891  
Patent No. 6680379  
GENERAL INFORMATION:  
APPLICANT: SUN, WILLIAM  
TITLE OF INVENTION: ORGANIC ANION TRANSPORTER GENES AND PROTEINS  
FILE REFERENCE: 030727.0022.CIP.1  
CURRENT APPLICATION NUMBER: US/09/614,891  
CURRENT FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: 60/143,771  
PRIOR FILING DATE: 1999-07-12  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 10  
LENGTH: 542  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-614-891-10

Query Match 35.0%; Score 42; DB 2; Length 542;  
Best Local Similarity 72.7%; Pred. No. 90;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FSCLLLTSEI 16  
Db 426 FSCFLYTSYL 436

## RESULT 10

US-09-902-540-15112  
Sequence 15112, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 15112  
LENGTH: 338  
TYPE: PRT  
ORGANISM: Myxococcus xanthus  
US-09-902-540-15112

Query Match 34.6%; Score 41.5; DB 2; Length 338;  
Best Local Similarity 40.0%; Pred. No. 63;  
Matches 8; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 MARG-FCSCLLLTSEIDL 19  
:|||||:|:|:|  
Db 73 IAPRNLVSCLAITDKLIFP 92

## RESULT 11

US-09-489-039A-12316  
; Sequence 12316, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 12316  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-12316

Query Match 34.2%; Score 41; DB 2; Length 113;  
Best Local Similarity 75.0%; Pred. No. 21;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARGFCSCLLLT 12  
:|||||:|:|:|  
Db 65 VARGFSTLL 76

## RESULT 12

US-09-489-039A-9041  
; Sequence 9041, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 9041  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-9041

Query Match 34.2%; Score 41; DB 2; Length 155;  
Best Local Similarity 36.8%; Pred. No. 30;  
Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 4 RGFSCLLTSEIDL 22  
:|:|:|:|:|:|:|:|:|  
Db 12 QGVSCVVGWTKXLSMSTKR 30

## RESULT 13

US-09-182-145-19  
; Sequence 19, Application US/09182145B  
; Patent No. 6387657  
; GENERAL INFORMATION:  
; APPLICANT: Botstein, David A.  
; APPLICANT: Cohen, Robert  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Lawrence, David A.  
; APPLICANT: Levine, Arnold J.  
; APPLICANT: Pennica, Diane  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: MISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: P1176R2  
; CURRENT APPLICATION NUMBER: US/09/182,145B  
; CURRENT FILING DATE: 1998-10-29  
; EARLIER APPLICATION NUMBER: US 60/063,704  
; EARLIER FILING DATE: 1997-10-29  
; EARLIER APPLICATION NUMBER: US 60/073,612  
; EARLIER FILING DATE: 1998-02-04  
; EARLIER APPLICATION NUMBER: US 60/081,695  
; EARLIER FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 156  
; SEQ ID NO 19  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-182-145-19

Query Match 34.2%; Score 41; DB 2; Length 228;  
Best Local Similarity 46.7%; Pred. No. 48;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 5 GFSCCLLTSEIDL 19  
:|:|:|:|:|:|:|:|:|  
Db 104 GFCTPLCSEVDVRLP 118

## RESULT 14

US-09-182-145-99  
; Sequence 99, Application US/09182145B  
; Patent No. 6387657  
; GENERAL INFORMATION:  
; APPLICANT: Botstein, David A.  
; APPLICANT: Cohen, Robert  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Lawrence, David A.  
; APPLICANT: Levine, Arnold J.  
; APPLICANT: Pennica, Diane  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: MISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: P1176R2  
; CURRENT APPLICATION NUMBER: US/09/182,145B  
; CURRENT FILING DATE: 1998-10-29  
; EARLIER APPLICATION NUMBER: US 60/063,704  
; EARLIER FILING DATE: 1997-10-29  
; EARLIER APPLICATION NUMBER: US 60/073,612  
; EARLIER FILING DATE: 1998-02-04  
; EARLIER APPLICATION NUMBER: US 60/081,695  
; EARLIER FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 156  
; SEQ ID NO 99  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-182-145-99

Query Match 34.2%; Score 41; DB 2; Length 229;  
Best Local Similarity 46.7%; Pred. No. 48;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 5 GFSCCLLTSEIDL 19  
:|:|:|:|:|:|:|:|:|  
Db 105 GFCTPLCSEVDVRLP 119



RESULT 15  
US-09-182-145-98  
; Sequence 98, Application US/09182145B  
; Patent NO. 6387657  
; GENERAL INFORMATION:  
; APPLICANT: Botstein, David A.  
; APPLICANT: Cohen, Robert  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Lawrence, David A.  
; APPLICANT: Levine, Arnold J.  
; APPLICANT: Pennica, Diane  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: P1176R2  
; CURRENT APPLICATION NUMBER: US/09/182,145B  
; CURRENT FILING DATE: 1998-10-29  
; EARLIER APPLICATION NUMBER: US 60/063,704  
; EARLIER FILING DATE: 1997-10-29  
; EARLIER APPLICATION NUMBER: US 60/073,612  
; EARLIER FILING DATE: 1998-02-04  
; EARLIER APPLICATION NUMBER: US 60/081,695  
; EARLIER FILING DATE: 1998-04-14  
; NUMBER OF SEQ ID NOS: 156  
; SEQ ID NO 98  
; LENGTH: 230  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-182-145-98

Query March 34.2%; Score 41; DB 2; Length 230;  
Best Local Similarity 46.7%; Pred. No. 48;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
QY 5 GFSCLLLTSEIDLP 19  
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Db 106 GFTCLPLCSEIDVRLP 120

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Job time : 4.288 secs

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OM protein - protein search, using sw model

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(Without alignments)  
736.353 Million cell updates/sec

Title: US-10-517-956-1

Perfect score: 1817

Sequence: 1 METNFSPTNEXEBSVESA.....TNDTANASAPPAETLQAM 351

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Searched: 283416 seqs, 96216763 residues

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Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1318	72.5	353	2 A42009	FMPLP-related recep
3	1249.5	68.8	350	2 A42009	N-formyl peptide r
4	1223.5	67.3	352	2 A46520	N-formyl peptide r
5	1174.5	64.6	364	2 A49542	N-formyl peptide c
6	538.5	29.6	371	2 JCS498	G protein-coupled
7	530.5	29.2	473	2 JCS835	anaphylatoxin C3a
8	513	28.2	350	1 A37963	complement C5a ana
9	509.5	28.0	482	2 S65766	G protein-coupled
10	502.5	27.7	371	2 JCS796	probable chemotatr
11	502	27.6	353	2 JCS2492	G protein-coupled
12	500	27.5	352	1 S27357	complement C5a ana
13	499	27.5	355	2 A55733	G protein-coupled
14	457.5	25.2	351	1 A46525	complement C5a ana
15	430.5	23.7	359	2 JCS2134	angiotensin II rec
16	427.5	23.5	359	2 JH0611	angiotensin II rec
17	426.5	23.5	359	2 JCS1104	angiotensin II rec
18	426.5	23.5	360	2 A51611	interleukin-8 rece
19	423.5	23.3	359	2 S15493	angiotensin II rec
20	422.5	23.3	355	2 JQ1231	interleukin-8 rece
21	420.5	23.1	359	2 JQ1516	angiotensin II rec
22	420.5	23.1	359	2 A42656	angiotensin II rec
23	419.5	23.1	352	2 A45747	neuropeptide Y/pep
24	418.5	23.0	359	2 JCS418	angiotensin II rec
25	418.5	23.0	359	2 A48425	angiotensin II rec
26	418	22.8	359	2 S44657	angiotensin II rec
27	413.5	22.8	352	2 G00068	elusin (LSTRA) - c
28	413.5	22.8	359	2 JCS194	angiotensin II rec
29	412	22.7	362	2 A30341	G protein-coupled

30	411.5	22.6	353	2 S28787	neuropeptide Y/pep
31	411.5	22.6	362	2 UN0694	angiotensin II rec
32	405.5	22.3	359	2 I51372	angiotensin II rec
33	405	22.3	418	2 A46226	somatostatin recep
34	403	22.2	359	2 A48921	interleukin-8 rece
35	402	22.1	398	2 I56517	mu opioid receptor
36	402	22.1	428	2 S30508	probable G protein
37	401	22.1	356	2 S42096	interleukin-8 rece
38	401	22.1	358	2 A53752	interleukin-8 rece
39	401	22.1	398	2 A57510	mu opioid receptor
40	399.5	22.0	350	2 A39445	interleukin-8 rece
41	399.5	22.0	391	2 A41795	somatostatin recep
42	399.5	22.0	391	2 C41795	somatostatin recep
43	399.5	22.0	391	2 A39297	mu opioid receptor
44	397	21.8	398	2 I56504	mu opioid receptor
45	396	21.8	392	2 S65693	opioid receptor mu

#### ALIGNMENTS

RESULT 1  
B42009  
FMPLP-related receptor 1 - human  
N/Alternate names: FMPLP receptor homolog FPR2; formyl peptide receptor like-1; probable C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence revision 14-Jul-1995 #text change 09-Jul-2004  
C/Accession: B42009; JCI258; JQ1521; A42492; I54751; S21581  
R/Bao, L.; Gerard, N.P.; Rddy Jr., R.L.; Shows, T.B.; Gerard, C.  
Genomics 13, 437-440, 1992  
A/Title: Mapping of genes for the human C5a receptor (C5AR), human FMPLP receptor (FPR), A/Reference number: A42009; MUID:92307681; PMID:1612600  
A/Accession: B42009  
A/Status: nucleic acid sequence not shown  
A/Molecule type: DNA  
A/Residues: 1-263, 'A', 265-338, 'C', 340-351 <BAO>  
A/Cross-references: UNIPROT:P25090; UNIPARC:UPI0000177808; GB:M76672  
A/Note: Authors translated the codons GTG for residue 15 as Glu, TCT for residue 19 as Tr  
R/Perez, H.D.; Holmes, R.; Kelly, E.; McClary, J.; Andrews, W.H.  
Gene 118, 303-304, 1992  
A/Title: Cloning of a cDNA encoding a receptor related to the formyl peptide receptor of A/Reference number: JCI258; MUID:92380523; PMID:1511907  
A/Accession: JCI258  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-351 <PER>  
A/Cross-references: UNIPARC:UPI00000012D0; EMBL:X63819; NID:g31460; PID:g31461  
A/Experimental source: bone marrow mRNA  
R/Ye, R.D.; Cavanagh, S.L.; Quehenberger, O.; Prossnitz, E.R.; Cochran, C.G.  
Biochem. Biophys. Res. Commun. 184, 582-589, 1992  
A/Title: Isolation of a cDNA that encodes a novel granulocyte N-formyl peptide receptor. A/Reference number: JQ1521; MUID:92246937; PMID:1374236  
A/Accession: JQ1521  
A/Molecule type: mRNA  
A/Residues: 1-351 <YE2>  
A/Cross-references: UNIPARC:UPI00000012D0; GB:M88107; NID:g189862; PID:g189863  
A/Experimental source: granulocytes  
A/Note: formyl peptide-stimulated calcium mobilization comparable to that of the formyl I R/Murphy, P.M.; Ozcelik, T.; Kenney, R.T.; Tiffany, H.L.; McDermott, D.; Francke, U.  
J. Biol. Chem. 267, 7637-7643, 1992  
A/Title: A structural homologue of the N-formyl peptide receptor. Characterization and c A/Reference number: A42492; MUID:92218423; PMID:1373134  
A/Accession: A42492  
A/Molecule type: mRNA  
A/Residues: 1-351 <MUR>  
A/Cross-references: UNIPARC:UPI00000012D0; GB:M84562; NID:g182741; PINN:AAA52473.1; PID:g A/Note: Sequence extracted from NCBI backbone (NCBIN:94159, NCBIPI:94150)  
R/Nomura, H.; Nielsen, B.W.; Matsushima, K.  
Int. Immunol. 5, 1239-1249, 1993  
A/Title: Molecular cloning of cDNAs encoding a IJ78 receptor and putative leukocyte chem A/Reference number: I54751; MUID:94092629; PMID:7505609  
A/Accession: I54751  
A/Status: preliminary; translated from GB/EMBL/DBJ

A,Molecule type: mRNA  
 A,Residues: 1-351 <RSS>  
 A,Cross-references: UNIPARC:UPI000000120D; GB:D10922; NID:g219864; PIDN:BA01720.1; PID:  
 C,Comment: This G-protein coupled receptor, homologous to the N-formyl peptide receptor  
 differentiatel myeloid cells and is probably a chemotactic receptor for some other ligand  
 C,Genetics:  
 A,Gene: GDB:FPRL1  
 A,Cross-references: GDB:127554; OMIM:136538  
 A,Map position: 19q13.3-19q13.4  
 A,Intons: #status absent  
 C,Superfamily: vertebrate rhodopsin  
 C,Keyword: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein  
 F:27-53/Domain: transmembrane #status predicted <TM1>  
 F:59-83/Domain: transmembrane #status predicted <TM2>  
 F:100-121/Domain: transmembrane #status predicted <TM3>  
 F:145-169/Domain: transmembrane #status predicted <TM4>  
 F:206-226/Domain: transmembrane #status predicted <TM5>  
 F:242-266/Domain: transmembrane #status predicted <TM6>  
 F:282-307/Domain: transmembrane #status predicted <TM7>  
 F:4/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:98-176/Dissulfide bonds: #status predicted

Query Match 100.0%; Score 1817; DB 2; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 5, 4e-145;  
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEXBEVSYESAGYTVLRILPLVVLGTVFVLGVLGVLVWAGFRMTRTVT 60  
 DB 1 METNFTPLNEXBEVSYESAGYTVLRILPLVVLGTVFVLGVLGVLVWAGFRMTRTVT 60  
 QY 61 TTCYLNALADSFSTATLPELVSMANGKMPGWLCKLHIVVDINLFGSVFLIGFLA 120  
 DB 61 TTCYLNALADSFSTATLPELVSMANGKMPGWLCKLHIVVDINLFGSVFLIGFLA 120  
 QY 121 LDRICVLHPVMAQNRTVSLAMKVIVGPIIALVTLVPVFLFTVTPINSDTYCTFNF 180  
 DB 121 LDRICVLHPVMAQNRTVSLAMKVIVGPIIALVTLVPVFLFTVTPINSDTYCTFNF 180  
 QY 181 ASWGTPEERLKVATIMLTARGIIRFVIGSLPMSIVACGLIAKIHKKGMKSSRPL 240  
 DB 181 ASWGTPEERLKVATIMLTARGIIRFVIGSLPMSIVACGLIAKIHKKGMKSSRPL 240  
 QY 241 RVTAVVASFICWPPFQVALGTVLWKLKMLFYGKKYIIDLVNPTSSLAFFNSCLNPM 300  
 DB 241 RVTAVVASFICWPPFQVALGTVLWKLKMLFYGKKYIIDLVNPTSSLAFFNSCLNPM 300  
 QY 301 LVFVGGDPRERLIHSLPTELRALSEDSAPTNDTANASPPAETELQAM 351  
 DB 301 LVFVGGDPRERLIHSLPTELRALSEDSAPTNDTANASPPAETELQAM 351

# RESULT 2

\* C42009  
 FMLP-related receptor 2 - human  
 N,Alternate names: FMLP-related receptor 1; probable chemotactic receptor FPRH2  
 C,Species: Homo sapiens (man)  
 C,Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
 C,Accession: C42009  
 R,Bao, L.; Gerard, N.P.; Bddy Jr., R.L.; Shows, T.B.; Gerard, C.  
 Genomics 13, 437-440, 1992  
 A,Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR),  
 A,Reference number: A42009; MUID:92307681; PMID:1612600  
 A,Accession: C42009  
 A,Status: nucleic acid sequence not shown  
 A,Molecule type: DNA  
 A,Residues: 1-353 <BAO>  
 A,Cross-references: UNIPROT:P25089; UNIPARC:UPI0000050485; GB:M76673; NID:g182668; PID:g  
 C,Comment: This Fmet-Leu-Phe receptor homolog, whose ligand is not yet known, appears to  
 C,Genetics:  
 A,Gene: GDB:FPRL2  
 A,Cross-references: GDB:128855; OMIM:136539  
 A,Map position: 19q13.3-19q13.4  
 A,Intons: #status absent

C,Superfamily: vertebrate rhodopsin  
 C,Keyword: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein  
 Query Match 72.5%; Score 1318; DB 2; Length 353;  
 Best Local Similarity 71.7%; Pred. No. 4e-103;  
 Matches 253; Conservative 39; Mismatches 59; Indels 2; Gaps 1;

QY 1 METNFTPLNEXBEVSYESAGYTVLRILPLVVLGTVFVLGVLGVLVWAGFRMTRTVT 60  
 DB 1 METNFTPLNEXBEVSYESAGYTVLRILPLVVLGTVFVLGVLGVLVWAGFRMTRTVT 60  
 QY 61 TTCYLNALADSFSTATLPELVSMANGKMPGWLCKLHIVVDINLFGSVFLIGFLA 120  
 DB 61 TTCYLNALADSFSTATLPELVSMANGKMPGWLCKLHIVVDINLFGSVFLIGFLA 120  
 QY 121 LDRICVLHPVMAQNRTVSLAMKVIVGPIIALVTLVPVFLFTVTPINSDTYCTFNF 180  
 DB 121 LDRICVLHPVMAQNRTVSLAMKVIVGPIIALVTLVPVFLFTVTPINSDTYCTFNF 180  
 QY 181 ASWGTPEERLKVATIMLTARGIIRFVIGSLPMSIVACGLIAKIHKKGMKSSRPL 240  
 DB 181 ASWGTPEERLKVATIMLTARGIIRFVIGSLPMSIVACGLIAKIHKKGMKSSRPL 240  
 QY 241 RVTAVVASFICWPPFQVALGTVLWKLKMLFYGKKYIIDLVNPTSSLAFFNSCLNPM 300  
 DB 241 RVTAVVASFICWPPFQVALGTVLWKLKMLFYGKKYIIDLVNPTSSLAFFNSCLNPM 300  
 QY 301 LVFVGGDPRERLIHSLPTELRALSE--DSAPTNDTANASPPAETELQAM 351  
 DB 301 LVFVGGDPRERLIHSLPTELRALTEVDS--QTSNTHTSAPPEETELQAM 353

# RESULT 3

A42009  
 N-formyl peptide receptor - human  
 N,Alternate names: FMP receptor  
 C,Species: Homo sapiens (man)  
 C,Date: 30-Sep-1993 #sequence\_revision 14-Jul-1995 #text\_change 09-Jul-2004  
 C,Accession: J02014; A36309; A35495; A42009; I52414  
 R,Murphy, P.M.; Tiffany, H.L.; McDermott, D.; Ahuja, S.K.  
 Gene 133, 285-290, 1993  
 A,Title: Sequence and organization of the human N-formyl peptide receptor-encoding gene.  
 A,Reference number: J02014; MUID:94040825; PMID:8224916  
 A,Accession: J02014  
 A,Molecule type: mRNA  
 A,Residues: 1-350 <MUR>  
 A,Cross-references: UNIPROT:P21462; UNIPARC:UPI000016A92F; GB:L10820; NID:g182739; PIDN:  
 A,Note: 192-Asn was also found  
 R:Boulay, F.; Tardif, M.; Brochon, L.; Vignais, P.  
 Biochemistry 29, 11123-11133, 1990  
 A,Title: The human N-formylpeptide receptor. Characterization of two cDNA isolates and  
 A,Reference number: A36309; MUID:91105045; PMID:2176894  
 A,Accession: A36309  
 A,Status: not compared with conceptual translation  
 A,Molecule type: mRNA  
 A,Residues: 1-191, 'N', 193-345, 'E', 347-350 <BOU1>  
 A,Note: the sequence in Genbank entry HUNNPPR, release 112.0, (PIDN:AAA3632.1) has the  
 R,Bao, L.; Gerard, N.P.; Bddy Jr., R.L.; Shows, T.B.; Gerard, C.  
 Genomics 13, 437-440, 1992  
 A,Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR),  
 A,Reference number: A42009; MUID:92307681; PMID:1612600  
 A,Accession: A42009  
 A,Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A,Molecule type: DNA

A;Residues: 1,'G',3-28,30-100,'L',102-104,106-112,'FLR',115-176,178-182,184-191,'N',194  
 A;Cross-references: UNIPARC:UPI00001778DA  
 R;Perez, H.D.; Holme, R.; Kelly, E.; McClary, J.; Chou, Q.; Andrews, W.H.  
 Biochemistry 31, 11595-11599, 1992  
 A;Title: Cloning of the gene coding for a human receptor for formyl peptides. Characteri  
 A;Reference number: 152414; MUID:93075765; PMID:1445895  
 A;Accession: 152414  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-5 <PER>  
 A;Cross-references: UNIPARC:UPI000011BA63; GB:649810; NID:g260832; PIDN:AAD14906.1; PID:  
 C;Genetic8  
 A;Gene: GDB:PPRI  
 A;Cross-references: GDB:127999; OMIM:136537  
 A;Map position: 19q13.4-19q13.4  
 A;Intons: #status absent  
 A;Note: entire coding region is found in exon 3; alternatively spliced mRNA transcripts  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein  
 F;27-53/Domain: transmembrane #status predicted <TM1>  
 F;59-83/Domain: transmembrane #status predicted <TM2>  
 F;100-121/Domain: transmembrane #status predicted <TM3>  
 F;145-169/Domain: transmembrane #status predicted <TM4>  
 F;206-225/Domain: transmembrane #status predicted <TM5>  
 F;242-266/Domain: transmembrane #status predicted <TM6>  
 F;279-304/Domain: transmembrane #status predicted <TM7>  
 F;4.10/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;98-176/Distufide bonds: #status predicted

Query Match 68.8%; Score 1249.5; DB 2; Length 350;  
 Best Local Similarity 68.9%; Pred. No. 2.2e-97;  
 Matches 241; Conservative 37; Mismatches 71; Indels 1; Gaps 1;

QY 1 METNFSPTLNEYEVESAGYTVLRILPLVVLGVTVLGNGLVIVWAGPFRMTVT 60  
 DB 1 METNSSLPTNISGTPVAVSGYLFLLITTVLVPVTVLGLGGLVWAGPFRMTVT 60  
 QY 61 TICLYNLALADFSFTATLPPLIVSMAMGEKMPFGMLCKLHIIVDINLFGSVFLIGFIA 120  
 DB 61 TISLYNLALADFSFTSTLPFPFVWAKGMHPGFMCKPFTVIDINLFGSVFLIALIA 120  
 QY 121 LDRICVLAHPVMAQNHRVSLAMKVIYVGPWIALVLTLPVFLFTVTTIPNGDTYCTFNF 180  
 DB 121 LDRVCVLAHPVMTNHRVSLAKKVIYIGPWWALLTLPLVIRVTPGKTYVACTFNF 180  
 QY 121 LDRICVLAHPVMAQNHRVSLAMKVIYVGPWIALVLTLPVFLFTVTTIPNGDTYCTFNF 180  
 DB 121 LDRVCVLAHPVMTNHRVSLAKKVIYIGPWWALLTLPLVIRVTPGKTYVACTFNF 180  
 QY 181 ASWCGTPEERLKVATIMLTARGIIRFVIGFSLPMSIYACGLIAAKIHKMKIKSSRPL 240  
 DB 181 SPWTDNPKERIKVAVMLTVRGIIRFVIGFSPMSIYAVSGLIATKIHKGGLIKSSRPL 240  
 QY 241 RVLTAVVASPFIQWPFQVALLGLTWLKEMLFYGKTKIIDILVNPSSLAFFNSCLNPM 300  
 DB 241 RVLSFVAAPFLCSPYQVALLITVAIRRELL-QGMKEIGIADVLSALAFNSCLNPM 299  
 QY 301 LVYFVGQDFRRLIHSPTSLERALSDESAFTNTAANSAPPATELQIA 350  
 DB 300 LVYFVGQDFRRLIHSPTSLERALSDESAFTNTAANSAPPATELQIA 349

## RESULT 4 -

A46520  
 N-formyl peptide receptor - rabbit  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C;Accession: A46520  
 R;He, R.D.; Quehenberger, O.; Thomas, K.M.; Navarro, J.; Cavanagh, S.L.; Prosenitz, E.R.  
 J. Immunol. 150, 1383-1394, 1993  
 A;Title: The rabbit neutrophil N-formyl peptide receptor. cDNA cloning, expression, and  
 A;Reference number: A46520; MUID:93163563; PMID:8432984  
 A;Accession: A46520  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: nucleic acid  
 A;Residues: 1-352 <YLI>  
 A;Cross-references: UNIPROT:Q05394; UNIPARC:UPI000012AA43; GB:M94549; NID:g165027; PIDN:

A;Experimental source: NZM, neutrophils  
 A;Note: sequence extracted from NCBI backbone (NCBIP:124908)  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 67.3%; Score 1223.5; DB 2; Length 352;  
 Best Local Similarity 67.7%; Pred. No. 3.4e-95;  
 Matches 239; Conservative 41; Mismatches 70; Indels 3; Gaps 2;

QY 1 METNFSPTLNEYEVESAGYTVLRILPLVVLGVTVLGNGLVIVWAGPFRMTVT 60  
 DB 1 MDNSSLPLNVSGTGATPRGLVLDVFSYLLVTFVGLGNGLVIVWAGPFRMTVT 60  
 QY 61 TICLYNLALADFSFTATLPPLIVSMAMGEKMPFGMLCKLHIIVDINLFGSVFLIGFIA 120  
 DB 61 TISLYNLALADFSFTSTLPFPFVWAKGMHPGFMCKPFTVIDINLFGSVFLIALIA 120  
 QY 121 LDRICVLAHPVMAQNHRVSLAMKVIYVGPWIALVLTLPVFLFTVTTIPN--GDTYCTF 178  
 DB 121 LDRICVLAHPVMAQNHRVSLAKKVIYIGPWWALLTLPLVIRVTPGKTYVACTF 180  
 QY 179 NPASWGTPEERLKVATIMLTARGIIRFVIGFSLPMSIYACGLIAAKIHKMKIKSSR 238  
 DB 181 DWSPTEDPKERIKVATIMLTARGIIRFVIGFSTPMSIYAVCGGLIATKIHKGGLIKSSR 240  
 QY 239 PLRVLTAVVASPFIQWPFQVALLGLTWLKEMLFYGKTKIIDILVNPSSLAFFNSCLN 298  
 DB 241 PLRVLSFVAAPFLCSPYQVALLITVAIRRELL-QGMKDLRIVDVTSFVAFNSCLN 299  
 QY 299 PMLYFVGQDFRRLIHSPTSLERALSDESAFTNTAANSAPPATELQIA 351  
 DB 300 PMLYFVGQDFRRLIHSPTSLERALSDESAFTNTAANSAPPATELQIA 352

## RESULT 5

A49542  
 N-formyl peptide chemotactic receptor - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
 C;Accession: A49542  
 R;Geo, J.L.; Murphy, P.M.  
 J. Biol. Chem. 268, 25395-25401, 1993  
 A;Title: Species and subtype variants of the N-formyl peptide chemotactic receptor reveal  
 A;Reference number: A49542; MUID:94064602; PMID:8244972  
 A;Accession: A49542  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-364 <GHO>  
 A;Cross-references: UNIPROT:P33766; UNIPARC:UPI00000210BF; GB:L22181; NID:g347396; PIDN:  
 C;Genetics:  
 A;Intons: #status absent  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: chemotaxis; transmembrane protein

Query Match 64.6%; Score 1174.5; DB 2; Length 364;  
 Best Local Similarity 64.6%; Pred. No. 4.6e-91;  
 Matches 237; Conservative 38; Mismatches 73; Indels 19; Gaps 5;

QY 1 METNFSPTLNEYEVESAGYTVLRILPLVVLGVTVLGNGLVIVWAG 52  
 DB 1 MDTNSSLNKKSAVNLNMGSGTQSVAGYIVLDVSYLLIFAVTFVGLVGNGLVIVWAG 60  
 QY 53 FRMTATVTTTCYANLALADFSFTATLPPLIVSMAMGEKMPFGMLCKLHIIVDINLFGS 112  
 DB 61 FRMKATVTTTISYANLALADFCFTSTLPFIYASVMGGMHPGFMCKPFTVIDINLFGS 120  
 QY 113 VFLLIGFIALDRICVLAHPVMAQNHRVSLAMKVIYVGPWIALVLTLPVFLFTVTTIPN- 171  
 DB 121 VFLLIALIADRICVLAHPVMAQNHRVSLAKKVIYIPWICAFPLTLPVIRLTTV--PNS 178  
 QY 172 ----GDTYCTFNPASWGTPEERLKVATIMLTARGIIRFVIGFSLPMSIYACGLIAAK 227  
 DB 179 RLDPGKTAFTDFSPWTKDPEERKVAIVMLTVRGIIRFVIGFSTPMSIYACGLIATK 238

```

Qy 228 IHKKMTKSSRPRLAVLTAVVASPFICMPPOVALVLTGVTWKEMLFYGKTKIIDLVNPT 287
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 239 IHKQGLTKSSRPRLVSPVVAAPFLCPCPOVALITITIOVRETKMTDGIYVAL-KIT 297
Qy 288 SSIAFPNSCLNPMLYVFGODFRERLTHSLPTSLERALSSESAPTNDTAAN---SASPPA 344
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 298 SPLAFNSCLNPMLYVFGODFRERLTHSLPASPALERALTEDSQTSDGTNLGNTSLS 357
Qy 345 ETELOAM 351
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 358 ENTLLNM 364

RESULT 6
G protein-coupled receptor DEZ - mouse
C/Species: Mus musculus (house mouse)
C/Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C/Accession: JCS498
R/Methner, A.; Hermey, G.; Schinke, B.; Hermans-Borgmeyer, I.
Biochem. Biophys. Res. Commun. 233, 336-342, 1997
A/Title: A novel G protein-coupled receptor with homology to neuropeptide and chemotact
A/Reference number: JCS498; MID:97289630; PMID:9144535
A/Contents: Brain
A/Accession: JCS498
A/Molecule type: mRNA
A/Residues: 1-371 <MET>
A/Cross-references: UNIPROT:P97468; UNIPARC:UPI00000269A9; GB:U79525; NID:g1732346; PIDN
C/Comment: This protein is involved in the bone metabolism.
P:110-187/Dileulide bonds: #status predicted

Query Match 29.6%; Score 538.5; DB 2; Length 371;
Best Local Similarity 35.2%; Pred. No. 1.1e-37;
Matches 120; Conservative 70; Mismatches 124; Indels 27; Gaps 8;

Qy 10 NEYEB-----VSYESAGYTLRLP--LVVLGVTFLVGLGNGLVIVWAGFPMRTVT 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 14 DEYSDGFGYVDDEKASPMERKAPVFLVIVSYLVCFLGLGNGLVIVATPFKKKTVM 73
Qy 62 ICYLNLAIDFSPTATPLFIVGMAGEKMPGMLCKLHIYVDINLPSSVFLIGFIL 121
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 74 VVWVNLAVDELFTNITPLPMHTTAAADYHWFPGAKCKISNPLSHMYTSVLLTVISF 133
Qy 122 DRCICVLHPWAQNRHTVSLAMKVIIVGPMIALVLTLPVFLPTVTIIPNGDYCTFNFA 181
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 134 DRCISVLLPFWGQNHSSIRLAVMTCSAVWLAFFLSPSLVFRDANI-HGKITCFNNIS 192
Qy 182 SWGCTPERLKAIVTMLTARG-----IIRFVIGFSLPMSTVAICGLIAKHKKGM 233
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 193 L--AADESSPHPHSGVSTGSRHVAVTTRFLCGFLIPVFIITACYLTIIVFKLQRNL 250
Qy 234 IKSSRLAVLTAVVASPFICMPPOVALVLTGVTWKEMLFYGKTKIIDLVNPTSSIAF 292
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 251 ANKKKPFKTIITITITIFPLCMCPYH-----TLYLBLEHTHTAVSSVSLGLPLATAVAI 304
Qy 293 FNSCLNPMLYVFGODFRERLTHSLPTSLERALSSESAPTN 333
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 305 ANSCNMPILYVFGHFRKFKV-ALTSRLANALSEDTPSS 344

RESULT 7
anaphylatoxin C3a receptor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C/Accession: JCS835
R/Fukuoka, Y.; Ember, J.A.; Hugli, T.E.
Biochem. Biophys. Res. Commun. 242, 663-668, 1998
A/Title: Cloning and characterization of rat C3a receptor: Differential expression of r
A/Reference number: JCS835; MID:98125550; PMID:946474
A/Accession: JCS835

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A/Molecule type: mRNA
A/Residues: 1-473 <FKU>
A/Cross-references: UNIPROT:O55197; UNIPARC:UPI0000126C12; GB:U86379; NID:g3015534; PIDN:
A/Experimental source: brain
C/Comment: This receptor plays a role in the central nervous systems.
C/Superfamily: vertebrate rhodopsin
C/Keywords: glycoprotein; phosphoprotein
F/22-51/Domain: transmembrane #status predicted <TM1>
F/58-83/Domain: transmembrane #status predicted <TM2>
F/138-160/Domain: transmembrane #status predicted <TM3>
F/322-347/Domain: transmembrane #status predicted <TM5>
F/367-392/Domain: transmembrane #status predicted <TM6>
F/406-430/Domain: transmembrane #status predicted
F/9,201/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/360/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 29.2%; Score 530.5; DB 2; Length 473;
Best Local Similarity 28.9%; Pred. No. 6.5e-37;
Matches 133; Conservative 60; Mismatches 107; Indels 161; Gaps 10;

Qy 27 ILPLVLGVTFLVGLGNGLVIVWAGFPMRTVTTCYLNLAIDFSPTATPLFLVSNMA 86
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 24 ISMWILSLTCLGLGNGLVIVWAGVKKRRTVNTVFLHLLADPLCCLSLPFSVAHLI 83
Qy 87 MGEKMPGMLCKLHIYVDINLPSSVFLIGFILADRCICVLHPWAQNRHTVSLAMKY 146
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 LKGMWYGLFLCKLPSVITILNMFASVFLTIAISDRCLMVKHKPIWCQNHRSVRTAFVC 143
Qy 147 VGPMLAVLTLPVFLPTVTIIPNGDY--CTPNPAS----- 182
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 144 GCWVVTFWMCIPVFVIRDLVW--DDYSCGYNFDSRAYDYMDYTNLSHLPINPD 200
Qy 183 -----N----- 183
Db 201 NSTGHVDRATASSSVAPARDLTATTAQSQTFHTSPEDPFSQDASQDPHYGKPTVL 260
Qy 184 -----GTPERLK----- 192
Db 261 IATIPGFVEBEHKSNTLNTGAFLSAHTERPSLTASSPLVYADFPDYPDQLMYGNHWT 320
Qy 193 --VAITMLARGLIIPVGFSLPMSTVAICGLIAKHKKMKIS-SRRLVLTAVVAS 249
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 321 PVALT-----ISRIVGFLVPPFMTCTSYLIVFRKNTLVSRNKTLLVAVAVTV 374
Qy 250 FFIQMPPOVALVLTGVTW-----LKEMLFYGKTKIIDLVNPTSSIAFPNSCLNPMLYV 304
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 375 FVCMIPHIIVGILLVITDQESALREVLPWDMSI-----ALASNSGCFNPFLVAL 426
Qy 305 VQODFRERLTHSLPTSLERALSSESAPTNDTAANSAPPAE 345
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 427 LKDPFRKKARQVKGILLEAFAFSEEL--THSTCTODKAPSK 465

RESULT 8
complement C5a anaphylatoxin receptor - human
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C/Accession: A37963; S13646; I52417; S30518
R/Boulay, F.; Merry, L.; Terdiffe, M.; Bouchon, L.; Vignais, P.
Biochemistry 30, 2993-2999, 1991
A/Title: Expression cloning of a receptor for C5a anaphylatoxin on differentiated HL-60 c
A/Reference number: A37963; MID:91175748; PMID:2007135
A/Accession: A37963
A/Molecule type: mRNA
A/Residues: 1-350 <BOU>
A/Cross-references: UNIPROT:P21730; UNIPARC:UPI0000000C99; GB:J05327; NID:g179699; PIDN:f
R/Gerard, N.P.; Gerard, C.
Nature 349, 614-617, 1991
A/Title: The chemotactic receptor for human C5a anaphylatoxin.
A/Reference number: S13646; MID:91156029; PMID:1847994
A/Accession: S13646

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A/Molecule type: mRNA  
A/Residues: 1-350 <GER>  
A/Cross-references: UNIPARC:UPI000000C99; EMBL:X58674; NID:929568; PIDN:CA837830.1; PID  
Biochem. Biophys. Res. Commun. 241, 390-394, 1997  
Biochemistry 32, 1243-1250, 1993  
A/Title: Human chemotaxin receptor genes cluster at 19q13.3-13.4. Characterization of th  
A/Reference number: 152417; MUID:93192225; PMID:8383526  
A/Accession: 152417  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-3 <RES>  
A/Cross-references: UNIPARC:UPI000011B869; GB:S56556; GB:S56557; NID:g298577; NID:g29857  
C/Genetic:  
A/Genes: GDB:CSRI; CSA; CSAR  
A/Cross-references: GDB:128856; OMIM:113995  
A/Map position: 19q13.3-19q13.4  
A/Introns: 1/3  
A/Note: the 1st of introns may be incomplete  
C/Function:  
A/Description: mediates the inflammatory and chemotactic responses of polymorphonuclear  
n  
C/Superfamily: vertebrate rhodopsin  
C/Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymor  
F/1-37/Domain: extracellular #status predicted <EX1>  
F/38-61/Domain: transmembrane #status predicted <TM1>  
F/62-71/Domain: intracellular #status predicted <IM1>  
F/72-94/Domain: transmembrane #status predicted <TM2>  
F/95-110/Domain: extracellular #status predicted <EX2>  
F/111-132/Domain: transmembrane #status predicted <TM3>  
F/133-149/Domain: intracellular #status predicted <IN2>  
F/150-174/Domain: transmembrane #status predicted <TM4>  
F/175-206/Domain: extracellular #status predicted <EX3>  
F/207-227/Domain: transmembrane #status predicted <TM5>  
F/228-243/Domain: intracellular #status predicted <IN3>  
F/243-264/Domain: transmembrane #status predicted <TM6>  
F/265-283/Domain: extracellular #status predicted <EX4>  
F/284-307/Domain: transmembrane #status predicted <TM7>  
F/308-350/Domain: intracellular #status predicted <IN4>  
F/5/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 28.2%; Score 513; DB 1; Length 350;  
Best Local Similarity 33.6%; Pred. No. 1,4e-35;  
Matches 122; Conservative 60; Mismatches 129; Indels 52; Gaps 9;

QY 4 NPSTP-LNEYEE-----VSYSAGYTVLRILPLVVGTVFVLGVLGNGLVIVVAGF 53  
DB 5 NYTPDYGHAYDDKOTDLNTPVDKTSNTLAKVPDILALVIVAVVFLVGVGLNVLVWYTA 64  
QY 54 RMTRTVTTICYNLALADFSFTATLPPLIVSMAMGKMPGWLCKLHIVDINLFGSV 113  
DB 65 EAKRTIVAWFNLAVADPISCLALPLFTSIYQHHMPPGGAACSLPDLILNVA 124  
QY 114 PLIGFIALDRCICYLHVVWQNHRTVSLANKVIVGPITLALVLTLPFLPLTYTTINGD 173  
DB 125 LLLATISADRFLLVFKPIWCONFRGAGLAWACAVAGLALLLPFLRVV-----RE 179  
QY 174 TY-----CTFNPAWSGTPDEBRKVALITWLTARGIIRFVIGSPISYIACGLIAAK 227  
DB 180 EYFPPKVLCAVDYSH-----DKRRERAV-----AIVRLVAGFLMPLITLTCTTFLLR 228  
QY 228 IHKKMKSRRPLRLTAVVAVASPFICWPPQVALLGTVLKMELFYGKYKIIDILVNPT 287  
DB 229 TWBRBATRSTKTKLVVAVAFPIPLPQVQVIM-----MSFLBPSPPFLINKL 281  
QY 288 SSU-----AFNSCLNPMLVYFVGODFRRLIHSPTLEALSDSA-----PTND 334  
DB 282 DSLCVSPAYINCINPIIYVAGGFGGRLRKSLPDLRLVLTESVYVSKSFTSTVD 341  
QY 335 TAA 337  
DB 342 TMA 344

RESULT 9  
S65766  
G protein-coupled receptor (clone AZ3B) - human  
C/Species: Homo sapiens (man)  
C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
A/Accession: S65766  
R/Roglic, A.; Prosenitz, E.R.; Cavanagh, S.L.; Pan, Z.; Zou, A.; Ye, R.D.  
Biochim. Biophys. Acta 1305, 39-43, 1996  
A/Title: cDNA cloning of a novel G protein-coupled receptor with a large extracellular l  
A/Reference number: S65766; MUID:96180983; PMID:8605247  
A/Accession: S65766  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-482 <ROG>  
A/Cross-references: UNIPROT:Q16581; UNIPARC:UPI0000126C11; EMBL:U28488; NID:91199577; P  
C/Superfamily: vertebrate rhodopsin  
C/Keywords: G protein-coupled receptor

Query Match 28.0%; Score 509.5; DB 2; Length 482;  
Best Local Similarity 26.6%; Pred. No. 3.8e-35;  
Matches 134; Conservative 59; Mismatches 117; Indels 193; Gaps 11;

QY 2 ETN-----FSPLNREBVSYSAGYTVLRILPLVVGTVFVLGVLGNGLVIVVAGFRMR 57  
DB 7 EINSSTLLSQPNNEPPV-----ILSNVILSTFLGLPENGVLWVAGLKMQR 54  
QY 58 TVTTTCYNLALADFSFTATLPPLIVSMAMGKMPGWLCKLHIVDINLFGSVFLIG 117  
DB 55 TVNTIWFHLTLADLCCSLPFLSLHNLALQGWPGFRLCKLIPSIIVLNMFASVFLLT 114  
QY 118 FIALDRCICYLHVVWQNHRTVSLANKVIVGPITLALVLTLPFLPLTYTTINGDTCR 177  
DB 115 AISLDRCLVLFKPIWCONHRNVGMACISGCIIVVAVFVVCIPVYVREIETTDNHR-CG 173  
QY 178 FNFA-----SW----- 183  
DB 174 YKGLSSLDYDPFYDPLNLSLENIYQRPGRMDRLPSSQTDNHPVTVPVQPOR 223  
QY 184 -----GGTPEE-----R 190  
DB 234 FQRPASDLPGRSARLTQNLVSNVFKPADVSPKIPSGPRIDHETSPLDNSDAFLSTH 293  
QY 191 LKV-----AIVMLTARGITRFVIGSLPMSIYA 218  
DB 294 LKLFPSASSNFYESLPGQFDYVNLGQFTDDQVPTPLVATITRLVVGFLPVSIMI 353  
QY 219 ICGLIAAKHKKMKTLS-SRPLRLTAVVAVASPFICWPPQVALLGTVLKMELFGKY 277  
DB 354 ACYSFTVFRQGRFPAKSSKTRFVAVVVAVFVLCWTPVHT-----F 396  
QY 278 KIDIIVNPTS-----SLAFNSCLNPMLVYFVGODFRRLIHSPTLSLR 323  
DB 397 GVSLTIDPETPLGKTLMSMDHVCIALAASGCFNFVALLGKDRKKARQSIGILBA 456  
QY 324 ALSED-----SAPTNDTAANSAS 341  
DB 457 AFSEELTRSTHCPSSNNVISERN 479

RESULT 10  
JC5796  
Probable chemoattractant receptor - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 24-Jan-1998 #sequence\_revision 13-Mar-1998 #text\_change 09-Jul-2004  
A/Accession: JC5796  
R/Owman, C.; Lolait, S.J.; Santen, S.; Olde, B.  
Biochem. Biophys. Res. Commun. 241, 390-394, 1997  
A/Title: Molecular cloning and tissue distribution of cDNA encoding a novel chemoattract  
A/Reference number: JC5796; MUID:98086361; PMID:9425281  
A/Accession: JC5796  
A/Molecule type: mRNA  
A/Residues: 1-371 <OMN>  
A/Cross-references: UNIPROT:Q35786; UNIPARC:UPI0000127BD5; DDBJ:A0002745; NID:g2624397; I

A:Experimental source: liver  
 C:Comment: This protein regulates the trafficking of immune cells during a microbial challenge  
 C:Superfamily: vertebrate rhodopsin  
 C/Keywords: glycoprotein; receptor; transmembrane protein  
 F:39-62/Domain: transmembrane #status predicted <TM1>  
 F:74-94/Domain: transmembrane #status predicted <TM2>  
 F:112-135/Domain: transmembrane #status predicted <TM3>  
 F:156-177/Domain: transmembrane #status predicted <TM4>  
 F:206-237/Domain: transmembrane #status predicted <TM5>  
 F:259-280/Domain: transmembrane #status predicted <TM6>  
 F:302-317/Domain: transmembrane #status predicted <TM7>  
 F:7,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.7%; Score 502.5; DB 2; Length 371;  
 Best Local Similarity 34.7%; Pred. No. 1,1e-34;  
 Matches 120; Conservative 63; Mismatches 124; Indels 39; Gaps 9;

QY 11 EYEE-----VSYSAG---YTVLRILPLVNLGVTVGLVNGLVYVWAGFPMRTVTYTTI 62  
 DB 15 EYSDGSDYIDLEBAGLEAKVAEVLVIVISLVCFGIIGNGLVIVIAIFPKMKKTNTV 74  
 QY 63 CYNLALADPSFTATLPFLIVSMAGKMPGFWFLCKLIHVVDINLFGSVFLIGFALD 122  
 DB 75 WPNVLAADVDFLPIFLPIHTTYAAMDHWFGKMKCISFSLSHMYTSVFLITVISFD 134  
 QY 123 RCICVLHPVWAQNRVTSIAMKVIYGFMLIALVLTLPFLPTVTI PNGDYCTFNFA 182  
 DB 135 RCISVLLPVSQNRHSVRLAVMTCVVVWVW-LSESPSLVFGHVSHTGKICFNNFSL 193  
 QY 183 WGGTPPE-----RLKVALTMLTARGITRFVGFSLPMSIVAICGLIAAKI 228  
 DB 194 --AAPEFSHSTRPDVPGVSRHVAVT-----VTRFLCGFLIPVETITACVLTIVFKL 245  
 QY 229 HKGKMKISRPRLVTLVAVSPFLCWPFPQVALLGTVMLEKMLFYGKYKIIDLVNP-T 287  
 DB 246 QRNRQAKTKKPKKIIITIIITFLCQCPH-----TLVLELHHTVAPASVSLGLPLA 299  
 QY 288 SSIAFNSCINPMLYVFGODPFRRLHSPTSLERALSDDAPTN 333  
 DB 300 TAVAIANSQNPILYVFMGHDPFKFKV-ALFSRLVNLSEDTPSS 344

RESULT 11  
 UC2492  
 G protein-coupled receptor 1 - rat  
 N:Alternate names: GPR-1  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 16-Mar-1995 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
 C/Accession: J02492  
 R:Marchese, A.; Cheng, R.; Lee, M.C.; Porter, C.A.; Heiber, M.; Goodman, M.; George, S.R. Biochem. Biophys. Res. Commun. 205, 1952-1958, 1994  
 A>Title: Mapping studies of two G protein-coupled receptor genes: An amino acid difference  
 A:Reference number: J02492; MIMD:95110347; PMID:7811287  
 A:Accession: J02492  
 A:Molecule type: mRNA  
 A:Residue: 1-353 <MAR>  
 A:Cross-references: UNIPROT:P46090; UNIPARC:UPI000012BA30; GB:S74702; NID:g786483; PIDN:  
 C:Superfamily: vertebrate rhodopsin  
 C/Keywords: glycoprotein; lipidprotein; phosphoprotein; receptor; thiolester bond; transmembrane  
 F:112-133/Domain: transmembrane #status predicted <TM2>  
 F:134-135/Region: DR motif  
 F:155-175/Domain: transmembrane #status predicted <TM3>  
 F:209-229/Domain: transmembrane #status predicted <TM4>  
 F:246-266/Domain: transmembrane #status predicted <TM5>  
 F:295-306/Domain: transmembrane #status predicted <TM6>  
 F:344-373/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:350-373/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted  
 F:330/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 27.6%; Score 502; DB 2; Length 353;  
 Best Local Similarity 34.2%; Pred. No. 1,2e-34;  
 Matches 114; Conservative 72; Mismatches 123; Indels 24; Gaps 8;

QY 4 NFSTPLNEY-EVVSYSAGYT-VLRILPLVNLGVTVGLVNGLVYVWAGFPMRTVTYTT 61  
 DB 14 NYSVALEYYSQEBDAEENYVPGIVHWISLLVLAALAVLAGIPGNAIYIWFPGFKKKTVTYTT 73  
 QY 62 ICYLNALADPSFTATLPFLIVSMAGKMPGFWFLCKLIHVVDINLFGSVFLIGFALD 121  
 DB 74 LWFNLALADPFLVFLPLVISTVSLSPFPMFLCKLNSFIAQLNMFSSVFLITVISL 133  
 QY 122 DRICVLHPVWAQNRVTSIAMKVIYGFMLIALVLTLPFLPTVTI PNGDYCTFNFA 181  
 DB 134 DRITHIHGSLSPHTLTKNSLIVL-FVNLILSLSGPFLYPRDYEV-NNRICANNQ 192  
 QY 182 SWGTPPEERLKVAILTMLTARGI--IRFVIGFSLPMSIVAICGLIAAKIHKGKMSRP 239  
 DB 193 EY-----ELTMRHHVLTWVLFELGYLLPLTMSCYCLIFKTKQNIILISSKH 242  
 QY 240 LRVTLVAVSPFLCWPFPQVALLGTVMLEKMLFYGKYKIIDLVNP-T 296  
 DB 243 LWMILSVLAIFWQWTFPHLF---SIW--ELSIHNSFQNVLOGGIPSLGLAFLNSC 296  
 QY 297 LNPMLYVFGODPFRRLHSPTSLERALSDD 329  
 DB 297 LNPILVITISKRFQARFASVAEVLKRSIMEAS 329

RESULT 12  
 S27357  
 Complement C5a anaphylatoxin receptor - dog  
 C/Species: Canis lupus familiaris (dog)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: S27357  
 R:Periet, J.; J.; Raspe, E.; Vaasart, G.; Parmentier, M. Biochem. J. 288, 911-917, 1992  
 A>Title: Cloning and functional expression of the canine anaphylatoxin C5a receptor. Evtc  
 A:Reference number: S27357; MIMD:93111969; PMID:1472004  
 A:Accession: S27357  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residue: 1-352 <PER>  
 A:Cross-references: UNIPROT:P30992; UNIPARC:UPI0000126C87; EMBL:X65860; NID:g878; PIDN:C  
 C/Function: mediates the inflammatory and chemotactic responses of polymorphonuclear  
 A:Description: mediates the inflammatory and chemotactic responses of polymorphonuclear  
 C:Superfamily: vertebrate rhodopsin  
 C/Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorph  
 F:1-38/Domain: extracellular #status predicted <EX1>  
 F:39-62/Domain: transmembrane #status predicted <TM1>  
 F:63-72/Domain: intracellular #status predicted <IM1>  
 F:73-95/Domain: transmembrane #status predicted <TM2>  
 F:96-111/Domain: extracellular #status predicted <EX2>  
 F:112-133/Domain: transmembrane #status predicted <TM3>  
 F:134-150/Domain: intracellular #status predicted <IM2>  
 F:151-175/Domain: transmembrane #status predicted <TM4>  
 F:176-208/Domain: extracellular #status predicted <EX3>  
 F:209-229/Domain: transmembrane #status predicted <TM5>  
 F:230-244/Domain: intracellular #status predicted <IM3>  
 F:245-266/Domain: transmembrane #status predicted <TM6>  
 F:267-285/Domain: extracellular #status predicted <EX4>  
 F:286-309/Domain: transmembrane #status predicted <TM7>  
 F:310-352/Domain: intracellular #status predicted <IM4>  
 F:5/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.5%; Score 500; DB 1; Length 352;  
 Best Local Similarity 31.3%; Pred. No. 1,7e-34;  
 Matches 113; Conservative 75; Mismatches 133; Indels 40; Gaps 7;  
 QY 4 NFSTP-----LNEYEVVSYSAGYTVLRILPLVNLGVTVGLVNGLVYVWAGFPMRTVTYTT 52  
 DB 5 NFSPPEYDPYGNATLDPNIFVDESINTPRLSPDMIALVIFPMVFLVGVGKFLVYVWVG 64  
 QY 53 FPMRTVTYTTICYNALADPSFTATLPFLIVSMAGKMPGFWFLCKLIHVVDINLFGS 112



Db 65 EVARTINAIWFLNIAVADLLSLALPILIFSSIIVOQGWPFGNACRIPLPSLILANVYAS 124

Qy 113 VFLLGFLIDBDCICYLHPVWAQNRHTVSLAKVIVGPMIILVYLTLPYEP--LTTVTIP 170

Db 125 ILLLTITTSADPFLVLFENPIWCONTRGPQLAAACSVAAVALTLTVSPFIRGHTIEYFP 184

Qy 171 NGDTYCTFNFAWGGTPEERLKVAILTMLTARG--IIRFVIGFSLPMISVALCYGLIAKI 228

Dp 185 FMMT-CGVDSGSGV-----VLVERGAAILRLMGFLGPLVLITISICYPLIIRT 231

Qy 229 HKKMIKRSRLRLVLTAVVASPFICWPPQVLALGTWMLKEMLPYGGYKIIDILVANPTS 288

Db 232 WSRKATRETKLTKLVAAVVASPFVLMPLPYQVTGMMALPYTHSGSFRRVSRHLSL---CV 288

Qy 289 SLAFNSCLANPMLVYFVQGDFFRERLIHSLPTSLERALSSEDA-----PTNDDTAMS 339

Db 289 AVAYINCCINPIIYVLAAGFHSRFLKSLPARLRQVLAESBVSVDGSDSKSITLSTVDTPAQ 348

Qy 340 A 340

Dp 349 S 349

RESULT 13  
A55733  
G protein-coupled receptor GPR1 - human  
C:Species: Homo sapiens (man)  
C:Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: A55733  
R:Marchase, A.; Docherty, J.M.; Nguyen, T.; Helber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, I.  
Genomic 23, 609-618, 1994  
A:Title: Cloning of human genes encoding novel G protein-coupled receptors.  
A:Reference number: A55733, MUID:95154831, PMID:7851889  
A:Accession: A55733  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-355 <MAR>  
A:Cross-references: UNIPROT:P46091, UNIPARC:UPI0000039D69, GB:U13666, NID:G577412, PIDN:  
C:Genetics:  
A:Gene: GDB:GPR1  
A:Cross-references: GDB:371707, OMIM:600239  
A:Map position: 15q25-15q26.1  
C:Superfamily: vertebrate rhodopsin  
;Keywords: G protein-coupled receptor

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Query Match      27.5%: Score 499; DB 2; Length 355;
Best Local Similarity 33.3%: Pred. No.2.1e-34;
Matches 115; Conservative 68; Mismatches 132; Indels 30; Gaps 7;

QY      1 MEIWPSTLNEYEEVSYESAGYT-----VLILRLVVLGVTVLGVGLNGSLVI 48
DB      1 MEDLEETLIFEEFENNSYDLDYYLSLESDLEEKQVLGVHWMSLVLYCLAFLVIGIGMAI VI 60

QY      49 WVAGFRMTRVTTTCYLNALADPSFTATLPLPLYSMMAMGKRPFGFLCGLHII VVDIN 108
DB      61 WFTGKMKKKVTVTTLMFLNLAIADFI FLFLPLDLYISYVMMNHMPGIIWLCRANSFTAQLN 120

QY      109 LGSVVELGLFALDQCIVLHPVMAQNHRSTSLMKVIVGSPMIILAVTLTLPVFLFTVT 168
DB      121 MPASVFFPLTVLISLDHYIHLIHPVLSHRHRLTNGSLIIFITWLLASLGLGFPALYFRDIVE 180

QY      169 IPNGDYCTFPFASGCTPBERLKAIVTMLTARGI--IRFYIGSLPMSIAVACGLIAA 226
DB      181 F-NHHTTLCYNF-----QKHDDLTLLIHHVLTWVKFIIGVLYFLPLTMSICVLCGIF 231

QY      227 KIHKKGMIKSSRPRLVLTAVVAASFICMPFPOLVALLCTWMLKEMLFYGTKK--ITDILV 284
DB      232 KYKKTATVLISSRHFWTILVVVVAFAVCWTPHYLF---SIW-ELTIHNSSSHVMQAGI 286

QY      285 NPTSSLAFPNGCLNPMLVVFGQDQRRRLHISLPTSLERALSDEQS 329
DB      287 PLSTGLAFLNGLCNLPILVYLISKKEQARFSSVAEILKTYTLMBS 331

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RESULT 14
A46525
complement C5a anaphylatoxin receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 10-Sep-1999
C:Accession: A46525
R:Gerard, C.; Bao, L.; Orozco, O.; Pearson, M.; Kunz, D.; Gerard, N.P.
J. Immunol. 149, 2600-2606, 1992
A:Title: Structural diversity in the extracellular faces of peptidergic G-protein-coupled
A:Reference number: A46525; MUID:93017861; PMID:1401897
A:Accession: A46525
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-351 <GBR>
A:Cross-references: UNIPARC:UPI00001637B6; GB:S46665; GB:L05630; NID:g257519; PIDD:AA8977
A:Experimental source: BALB/C
A>Note: sequence extracted from NCBI backbone (NCBIP:116075)
C:Function:
A:Description: mediates the inflammatory and chemotactic responses of polymorphonuclear
in granulocyte, macrophage, rhodocyt

```

n  
 C<sub>2</sub>Superfamily: vertebrate rhodopsin  
 CKeywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorph  
 F.1-37/Domain: extracellular #status predicted <EX1>  
 F.38-61/Domain: transmembrane #status predicted <TM1>  
 F.62-71/Domain: intracellular #status predicted <IM1>  
 F.72-94/Domain: transmembrane #status predicted <TM2>  
 F.95-110/Domain: extracellular #status predicted <EX2>  
 F.111-133/Domain: transmembrane #status predicted <TM3>  
 F.133-149/Domain: intracellular #status predicted <IM2>  
 F.150-174/Domain: transmembrane #status predicted <TM4>  
 F.175-207/Domain: extracellular #status predicted <EX3>  
 F.208-228/Domain: transmembrane #status predicted <TM5>  
 F.229-243/Domain: intracellular #status predicted <IM3>  
 F.244-265/Domain: transmembrane #status predicted <TM6>  
 F.266-284/Domain: extracellular #status predicted <EX4>  
 F.285-308/Domain: transmembrane #status predicted <TM7>  
 F.309-351/Domain: intracellular #status predicted <IM4>  
 F.6/Binding site: carboxylate (Asn) (covalent) #status predicted

	Query Match	25.2%	Score 457.5	DB 1	Length 351
	Best Local Similarity	31.8%	Pred. No. 6	3e-31	
	Matches	103	Conservative	62	Mismatches 136; Indels 23; Gaps 6;
QY	27 ILPLVLTGTVFLVGLNGSLVIYWAGFRMRTVTTCICYNLALADFSEFATLLPFLIYSMA	86			
DB	38 VVALIYSVFLVGVGNALVVMTAFEPDPSNAIMFLNALVDLLSCLMAPLFETVL	97			
QY	87 MGEKRPGEWFLCKLIHIVDINLFGSVPLGFIALDRICLYLHVMAQNHTVSILAMKYI	146			
DB	98 NHNMYFPATACTIYLPSSLILNMVASILLTLATTISADRELLPFKKIWCKVRGTGLAMNAC	157			
QY	147 VGPMITALLVLTLPVFLFTTY-TIPNDGYCTFNPMASGTPRERLKVAITMLTARGIIR	205			
DB	158 GVAVMALLLTIPTSPVRYEAKDPDYSEHTVCGINYG-GSFPEK-----AVALIKR	207			
QY	206 FVIGESLEMSIVAICYGLIAAKIHKKMGKISSRLPYLATAVASFFICMPFOUVALIGT	265			
DB	208 LMGVFVPLELINTLCYTFELLRMTSRKRTRSTKLKVMAVVICFEFIWMLEYQTGVGM-I	266			
QY	266 VWLKEMLFYKKYKIIDLVNPFTSSLAFFNSCLANPMILYFVGODPRERIHLSPISLEAL	325			
DB	267 AMLPPS--SPTLKEVEKLNLSLCVSLAYNNCCVNPIIYVMAGOGFHGRILRSLLPSIIRNAL	324			
QY	326 SEDSA-----PTNDTAANSA	340			
DB	325 SEDSGARDSKTFPTSDTSTRKS	348			

RESULT 15  
JC2134  
angiotensin II receptor type 1A - rat  
N;Alternate names: AT1a receptor; AT3 receptor



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:10:33 ; Search time 277.992 Seconds

(without alignments)  
890,819 Million cell updates/sec

Title: US-10-517-956-1

Perfect score: 1817

Sequence: 1 METNFTPTLNEYEVSYESA.....TNDTANASAPPAETIQAM 351

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_05.80.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1817	100.0	351	1 FPR1_HUMAN	P25090 homo sapien
2	1782	98.1	348	1 FPR1_PANTR	P79242 pan troglod
3	1781	98.0	348	1 FPR1_GORGO	P79177 gorilla gor
4	1744	96.0	348	1 FPR1_PONPY	P79236 pongo pygma
5	1740	95.8	348	1 FPR1_MACMU	P79190 macaca mula
6	1420	78.2	351	2 O88536_MOUSE	O88536 mus musculu
7	1337	73.6	351	1 FPR1_MOUSE	O88790 mus musculu
8	1327	73.0	353	2 O6L5J4_HUMAN	P25089 homo sapien
9	1327	73.0	353	2 O6L5J4_HUMAN	O6L5J4 homo sapien
10	1325	72.9	347	2 O88535_MOUSE	O88535 mus musculu
11	1312	72.2	349	1 FPR1_PANTR	P79243 pan troglod
12	1304	71.8	349	1 FPR1_PONPY	P79237 pongo pygma
13	1299	71.5	349	1 FPR1_GORGO	P79178 gorilla gor
14	1292	71.1	349	1 FPR1_MACMU	P79191 macaca mula
15	1243.5	68.4	350	1 FPR1_HUMAN	P21462 homo sapien
16	1225.5	67.4	346	1 FPR1_PANTR	P79241 pan troglod
17	1225.5	67.4	346	1 FPR1_PONPY	P79235 pongo pygma
18	1223.5	67.3	352	1 FPR1_RABIT	Q05394 coryctolagus
19	1206.5	66.4	346	1 FPR1_GORGO	P79176 gorilla gor
20	1206.5	66.4	346	1 FPR1_MACMU	P79189 macaca mula
21	1174.5	64.6	364	1 FPR1_MOUSE	P73766 mus musculu
22	1140.5	62.8	343	2 O88537_MOUSE	O88537 mus musculu
23	1107.5	61.0	323	2 O88538_MOUSE	O88538 mus musculu
24	1074.5	59.1	338	2 Q71M7_MOUSE	Q71M7 mus musculu
25	1074.5	59.1	340	2 Q8H290_SAGO	Q8H290 saguinus oe
26	1071.5	59.0	339	2 Q71M8_MOUSE	Q71M8 mus musculu
27	644	35.4	322	2 Q4SMX3_TETNG	Q4SMX3 tetodon n
28	585.5	32.2	322	2 Q4RSY3_TETNG	Q4RSY3 tetodon n
29	580.5	31.9	461	2 Q5Z1N6_CHICK	Q5Z1N6 gallus gall
30	553.5	30.5	356	1 GPR33_HUMAN	Q75388 homo sapien
31	553.5	30.5	356	2 Q502U7_HUMAN	Q502U7 homo sapien

32	548.5	30.2	475	1 C3AR_CANPO	O88680 cavia porce
33	543.5	29.9	356	2 Q6NWS5_HUMAN	Q6NWS5 homo sapien
34	542.5	29.9	477	1 C3AR_MOUSE	O09047 mus musculu
35	542.5	29.9	477	2 Q5U7A4_MOUSE	Q5U7A4 mus musculu
36	541.5	29.8	477	2 O8C6R2_MOUSE	O8C6R2 mus musculu
37	538.5	29.6	371	1 CML1_MOUSE	P97468 mus musculu
38	534.5	29.4	371	2 Q5U0H0_HUMAN	Q5U0H0 homo sapien
39	534.5	29.4	373	1 CML1_HUMAN	Q99788 homo sapien
40	530.5	29.2	382	1 GPR44_MOUSE	Q92236 mus musculu
41	530.5	29.2	382	2 Q54A00_MOUSE	Q54A00 mus musculu
42	530.5	29.2	473	1 C3AR_RAT	O55197 rattus norv
43	513	28.2	350	1 C5AR_HUMAN	P21730 homo sapien
44	509.5	28.0	482	1 C3AR_HUMAN	Q16581 homo sapien
45	509	28.0	403	2 Q6XKD3_RAT	Q6XKD3 rattus norv

#### ALIGNMENTS

RESULT 1	FPRL1_HUMAN	STANDARD;	PRT;	351 AA.
ID	FPRL1_HUMAN			
AC	P25090;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	FMPLP-related receptor 1 (FMPLP-R-1) (Lipoxin A4 receptor) (LXA4 receptor) (Formyl peptide receptor-like 1) (FPL) (HM63).			
GN	Name=FPRL1; Synonyms=PPR2, PPRH1, LXAAR;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=92307681; PubMed=1612600;			
RA	Bao L., Gerard N.P., Bddy R.L. Jr., Shows T.B., Gerard C.;			
RT	"Mapping of genes for the human C5a receptor (C5AR), human FMPLP receptor (FPLR), and two FMPLP receptor homologue orphan receptors (PPRH1, PPRH2) to chromosome 19.";			
RT	Genomics 13:437-440(1992).			
RL	[2]			
RN	NUCLEOTIDE SEQUENCE.			
RP	TISSUE=Bone marrow;			
RX	MEDLINE=9238053; PubMed=1511907; DOI=10.1016/0378-1119(92)90208-7;			
RA	Perez H.D., Holmes R., Kelly B., McClary J., Andrews W.H.;			
RT	"Cloning of a cDNA encoding a receptor related to the formyl peptide receptor of human neutrophils.";			
RT	Gene 118:303-304(1992).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Granulocyte;			
RX	MEDLINE=92246937; PubMed=1374236;			
RA	Ye R.D., Cavanagh S.L., Quehenberger O., Prossnitz E.R.;			
RT	Cochrane C.G.;			
RT	"Isolation of a cDNA that encodes a novel granulocyte N-formyl peptide receptor.";			
RT	Biochem. Biophys. Res. Commun. 184:582-589(1992).			
RL	[4]			
RN	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=92218423; PubMed=1371314;			
RA	Murphy P.M., Oseclik T., Kenney R.T., Tiffany H.L., McDermott D.,			
RT	Frankel U.;			
RT	"A structural homologue of the N-formyl peptide receptor.			
RT	Characterization and chromosome mapping of a peptide chemottractant receptor family.";			
RT	J. Biol. Chem. 267:7637-7643(1992).			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Monocyte;			
RX	MEDLINE=94092629; PubMed=7505609;			
RA	Nomura H., Nielsen B.W., Matsushima K.;			

RA	Serhan C.N.;
RT	"Aspirin-triggered 15-epi-lipoxin A <sub>4</sub> (LXA <sub>4</sub> ) and LXA <sub>4</sub> stable analogues
RL	are potent inhibitors of acute inflammation: evidence for anti-
RN	inflammatory receptors.";
RM	J. Exp. Med. 185:1693-1704(1997).
CC	-1- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
CC	which are powerful neutrophil chemotactic factors. Binding
CC	FMPL to the receptor causes activation of neutrophils. This
CC	response is mediated via a G-protein that activates a
CC	phosphatidylinositol-calciun second messenger system. The
CC	activation of LXAR could result in an anti-inflammatory outcome
CC	counteracting the actions of proinflammatory signals such as LTBA
CC	(leukotriene B <sub>4</sub> ).
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1- TISSUE SPECIFICITY: Expressed abundantly in the lung and
CC	neutrophils. Also found in the spleen and testis.
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics institute. There are no restrictions on its
CC	use as long as its content is in no way modified and this statement is not
CC	removed.
DR	EMBL; M76672; AAA58481.1; -; mRNA.
DR	EMBL; X63819; CAA45319.1; -; mRNA.
DR	EMBL; M88107; AAA60070.1; -; mRNA.
DR	EMBL; M84562; AAA52473.1; -; mRNA.
DR	EMBL; D10922; BAA01720.1; -; mRNA.
DR	EMBL; U81501; AA851133.1; -; mRNA.
DR	EMBL; AF054013; AAC13684.1; -; mRNA.
DR	EMBL; AY225226; AA067711.1; -; Genomic DNA.
DR	EMBL; AC018755; AA87844.1; -; Genomic DNA.
DR	EMBL; BC029125; AAH29125.1; -; mRNA.
DR	EMBL; BC071722; AAH71722.1; -; mRNA.
DR	PfR; B42009; B42009.
DR	HSSP; P34936; 1DDO.
DR	Ensembl; ENSG00000171049; Homo sapiens.
DR	HNCI; HGNC:3827; PPRL1.
DR	H-InvDB; HIX0019402; -.
MIM	136538; -.
DR	GO; GO:0016021; C:integral to membrane; TAS.
DR	GO; GO:0005886; C:plasma membrane; TAS.
DR	GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR	GO; GO:0004982; F:N-formyl peptide receptor activity; TAS.
DR	GO; GO:0007155; P:cell adhesion; TAS.
DR	GO; GO:0006928; P:cell motility; TAS.
DR	GO; GO:0006935; P:chemotaxis; TAS.
DR	GO; GO:0007186; P:G-protein coupled receptor protein signaln. ; TAS.
DR	GO; GO:0006954; P:inflammatory response; TAS.
DR	InterPro; IPR000826; Ptc/met receptor.
DR	InterPro; IPR000276; GPCR_Rhodopsn.
Pfam	PF00001; 7cm 1; 1.
PRINTS	PRO0526; FMELTDPHER.
DR	PRINTS; PRO0237; GPCRRHODOPSN.
DR	PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
DR	PROSITE; PS0262; G PROTEIN RECP FL 2; 1.
KW	Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor;
KW	Sensory transduction; Transducer; Transmembrane.
FT	TOPO_DOM 1 27
FT	TRANSMEM 28 50
FT	TRANSMEM 51 50
FT	TOPO_DOM 52 63
FT	TRANSMEM 61 81
FT	TRANSMEM 82 100
FT	TOPO_DOM 101 121
FT	TRANSMEM 122 140
FT	TOPO_DOM 141 162
FT	TRANSMEM 163 205
FT	TOPO_DOM 206 226
FT	TRANSMEM 227 242
FT	TOPO_DOM 243 266
FT	TRANSMEM 267 286
FT	TOPO_DOM 287 306
FT	TRANSMEM 306 306
RA	"Molecular cloning of cDNAs encoding a LJD8 receptor and putative
RT	leucocyte chemoattractant peptide receptors";
RL	Int. Immunol. 5:1239-1249(1993).
RN	[6]
RM	Nucleotide sequence.
RA	Maddox J.F., Haechicha M., Takano T., Petasis N.A., Fokin V.V.,
RA	Serhan C.N.;
RL	Submitted (Apr-1997) to the EMBL/GenBank/DDBJ databases.
RP	Nucleotide sequence [LARGE SCALE MENA].
RM	[7]
RA	MEBLINE=98251774; PubMed=9547339; DOI=10.1084/jem.187.8.1285;
RA	Gronett K., Gewirtz A., Madara J.L., Serhan C.N.;
RT	"Identification of a human enterocyte lipoxin A <sub>4</sub> receptor that is
RT	regulated by interleukin (IL)-13 and interferon gamma and inhibits
RT	tumor necrosis factor alpha-induced IL-8 release.";
RL	J. Exp. Med. 187:1285-1294(1998).
RN	[8]
RP	Nucleotide sequence [LARGE SCALE MENA].
RM	[9]
RA	Pubmed=15057824; DOI=10.1038/nature02359;
RA	Grimwood J.E., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA	Lamerind J.E., Hellsten U., Goodstein D., Coutrome O., Tiran-Guyamfi M.,
RA	Aerts A., Altherm M., Ashworth L., Bajorek E., Black S., Branscomb E.,
RA	Campbell S., Carrino A.V., Caolle C., Chan Y.M., Christensen M.,
RA	Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Deter J.C.,
RA	Escriba J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,
RA	Glavina T., Gomez M., Gonzales B., Groza M., Hammon N., Hawkins T.,
RA	Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
RA	Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
RA	Malaciti S., Martinez D., McCreedy P.M., Medina C., Morgan J.,
RA	Nelson K., Nolan M., Orchenko I., Pitluck S., Pollard M.,
RA	Popkie A.P., Predki P., Quan G., Ramirez U., Raeh S., Retterer J.,
RA	Rodriguez A., Rogers S., Salamon A., Salazar A., She X., Smith D.,
RA	Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Velazquez A.,
RA	Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
RA	Furey T.S., DeLong P., Dickson M., Gordon D., Richter E.B.,
RA	Pennachio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA	Rubin E.M., Lucas S.W.;
RT	"The DNA sequence and biology of human chromosome 19.";
RL	Nature 428:529-535(2004).
RN	[10]
RP	Nucleotide sequence [LARGE SCALE MENA].
RM	[11]
RA	MEBLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Collins E.A., Grout L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schlter G.D.,
RA	Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diacenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant P.L., Scheetz T.E.,
RA	Bromstein M.J., Udell T.B., Tochiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A.,

FT TOPO\_DOM 307 351 Cytoplasmic (Potential).  
 FT CARBOHYD 4 4 N-linked (GlcNAc...) (Potential).  
 Query Match 100.0%; Score 1817; DB 1; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-100;  
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEBEVSEYASGYTVLRILPLVLGVTFLVGLNGGLVIVAGFRMRTVT 60  
 DB 1 METNFTPLNEBEVSEYASGYTVLRILPLVLGVTFLVGLNGGLVIVAGFRMRTVT 60  
 QY 61 TICVLMALADFSFATLPLPLIVSMAMGKMPFGWFLCKLHIYVDINLFGSVPLIFIA 120  
 DB 61 TICVLMALADFSFATLPLPLIVSMAMGKMPFGWFLCKLHIYVDINLFGSVPLIFIA 120  
 QY 121 LDRICICVLPVMAQNHRTVSLAMKVIVGPMILAVLTLPVPLFTVTITNGDTCYTFNF 180  
 DB 121 LDRICICVLPVMAQNHRTVSLAMKVIVGPMILAVLTLPVPLFTVTITNGDTCYTFNF 180  
 QY 181 ASNGGTEPERLKVATITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMKSSRPL 240  
 DB 181 ASNGGTEPERLKVATITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMKSSRPL 240  
 QY 241 RVLTAVVASFPCWPFQVALLGTWVKEMLFYGYKXIIDIIVNPTSSLAFFNSCLNPM 300  
 DB 241 RVLTAVVASFPCWPFQVALLGTWVKEMLFYGYKXIIDIIVNPTSSLAFFNSCLNPM 300  
 QY 301 LVYFVGQDFRERLIHSLPTSLERLSEDSAPTNDTANASPPAETELQAM 351  
 DB 301 LVYFVGQDFRERLIHSLPTSLERLSEDSAPTNDTANASPPAETELQAM 351

RESULT 2  
 PPR1 PANTR STANDARD; PRT; 348 AA.  
 ID FPR1 PANTR STANDARD; PRT; 348 AA.  
 AC P79242;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE FMLP-related receptor I (FMLP-R-I) (Fragment).  
 GN Name=PPR1;  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Pan.  
 NCBI\_TaxID=9598;  
 RN NCBIOTIDE SEQUENCE.  
 RP MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;  
 RA Alvarez V., Coco E., Sehen F., Gonzalez-Koces S., Lopez-Larrea C.;  
 RT "Molecular evolution of the N-formyl peptide and Csa receptors in non-  
 human primates."; Immunogenetics 44:446-452(1996).  
 RL Immunogenetics 44:446-452(1996).  
 CC -1- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,  
 which are powerful neutrophils chemotactic factors. Binding of  
 FMLP to the receptor causes activation of neutrophils. This  
 response is mediated via a G-protein that activates a  
 phosphatidylinositol-calcium second messenger system.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC EMBL: X97739; CAA66323.1; -; Genomic DNA.  
 DR HSSP: P34996; 1DDP.  
 DR InterPro: IPR000826; Frc/met\_receptor.  
 DR InterPro: IPR000276; GPCR\_Rhodpm.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00526; FMETLEUPHER.

DR PRINTS; PR00237; GPCRHOPOEN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1;  
 DR PROSITE; PS50262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KM Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor;  
 KW Sensory transduction; Transducer; Transmembrane.  
 FT TOPO\_DOM 348 348  
 FT TRANSMEM 25 58  
 FT TOPO\_DOM 48 48  
 FT TRANSMEM 59 97  
 FT TOPO\_DOM 81 97  
 FT TRANSMEM 98 118  
 FT TOPO\_DOM 119 137  
 FT TRANSMEM 138 159  
 FT TOPO\_DOM 160 202  
 FT TRANSMEM 203 223  
 FT TOPO\_DOM 224 239  
 FT TRANSMEM 240 263  
 FT TOPO\_DOM 264 283  
 FT TRANSMEM 284 303  
 FT TOPO\_DOM 304 348  
 FT CARBOHYD 1 1  
 FT DISULFID 95 173  
 FT NON\_TER 1 1  
 FT NON\_TER 348 348  
 SQ SEQUENCE 348 AA; 38575 MW; 5587670DF4D594E CRC64;  
 Query Match 98.1%; Score 1782; DB 1; Length 348;  
 Best Local Similarity 98.9%; Pred. No. 1.9e-98;  
 Matches 344; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 NFSTPLNEBEVSEYASGYTVLRILPLVLGVTFLVGLNGGLVIVAGFRMRTVTTC 63  
 DB 1 NFSTPLNEBEVSEYASGYTVLRILPLVLGVTFLVGLNGGLVIVAGFRMRTVTTC 60  
 QY 64 YNLMALADFSFATLPLPLIVSMAMGKMPFGWFLCKLHIYVDINLFGSVPLIFIALDR 123  
 DB 61 YNLMALADFSFATLPLPLIVSMAMGKMPFGWFLCKLHIYVDINLFGSVPLIFIALDR 120  
 QY 124 CFCVLPVMAQNHRTVSLAMKVIVGPMILAVLTLPVPLFTVTITNGDTCYTFNFASW 183  
 DB 121 CFCVLPVMAQNHRTVSLAMKVIVGPMILAVLTLPVPLFTVTITNGDTCYTFNFASW 180  
 QY 184 GGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMKSSRPLRV 243  
 DB 181 GGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMKSSRPLRV 240  
 QY 244 TAVVASFPCWPFQVALLGTWVKEMLFYGYKXIIDIIVNPTSSLAFFNSCLNPMKY 303  
 DB 241 TAVVASFPCWPFQVALLGTWVKEMLFYGYKXIIDIIVNPTSSLAFFNSCLNPMKY 300  
 QY 304 FVGQDFRERLIHSLPTSLERLSEDSAPTNDTANASPPAETELQAM 351  
 DB 301 FVGQDFRERLIHSLPTSLERLSEDSAPTNDTANASPPAETELQAM 348

RESULT 3  
 PPR1 GORGO STANDARD; PRT; 348 AA.  
 ID FPR1 GORGO STANDARD; PRT; 348 AA.  
 AC P79177;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE FMLP-related receptor I (FMLP-R-I) (Fragment).  
 GN Name=PPR1;  
 OS Gorilla gorilla gorilla (Lowland gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Gorilla.  
 NCBI\_TaxID=9595;  
 RN NCBIOTIDE SEQUENCE.  
 RP MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;  
 RA Alvarez V., Coco E., Sehen F., Gonzalez-Koces S., Lopez-Larrea C.;

```

RT      "Molecular evolution of the N-formyl peptide and C5a receptors in non-
RL      human primates."; 44:446-452(1996).
CC      -1- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
CC      which are powerful neutrophils chemotactic factors. Binding of
CC      FMLP to the receptor causes activation of neutrophils. This
CC      response is mediated via a G-protein that activates a
CC      phosphatidylinositol-calcium second messenger system.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      HMBL; X97738; CAA66322.1; -; Genomic_DNA.
DR      HMBP; P34966; 1DDD.
DR      InterPro; IPR000826; Frc/met_receptor.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00526; FMETLEUPHER.
DR      PROSITE; PS00237; GPCR_RHODOPSIN.
DR      PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR      PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW      Sensory transduction; Transducer; Transmembrane.
FT      TOPO_DOM <1 24
FT      TRANSMEM 25 47
FT      TOPO_DOM 48 58
FT      TRANSMEM 59 80
FT      TOPO_DOM 81 97
FT      TRANSMEM 98 118
FT      TOPO_DOM 119 137
FT      TRANSMEM 138 159
FT      TOPO_DOM 160 202
FT      TRANSMEM 203 223
FT      TOPO_DOM 224 239
FT      TRANSMEM 240 263
FT      TOPO_DOM 264 283
FT      TRANSMEM 284 303
FT      TOPO_DOM 304 348
FT      CARBOHYD 1 1
FT      DISULFID 95 173
FT      NON_TER 1 1
FT      SEQUENCE 348 AA; 38581 MW; B1F0B3BDC76CAA0 CRC64;
SQ
Query Match      98.0%; Score 1781; DB 1; Length 348;
Best Local Similarity 98.9%; Pred. No. 2.2e-98;
Matches 344; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY      304 FVGDPRERLIHSLPTSLRALSEDSAPNTNDRANSAPPAETLQAM 351
DB      ||||||||||||||||||||||||||||||||||||||||||||
DB      301 FVGDPRERLIHSLPTSLRALSEDSAPNTNDRANSAPPAETLQAM 348
DB      ||||||||||||||||||||||||||||||||||||||||||||

RESULT 4
ID      FPR1_PONPY STANDARD; PRT; 348 AA.
AC      P79236;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      FMLP-related receptor I (FMLP-R-I) (Fragment).
GN      Name=FPR1;
OS      Pongo pygmaeus (Orangutan).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC      Pongo.
OX      NCBI_TaxId=9600;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;
RA      Alvarez V., Coto B., Sehen F., Gonzalez-Koces S., Lopez-Larrea C.;
RT      "Molecular evolution of the N-formyl peptide and C5a receptors in non-
RT      human primates."; 44:446-452(1996).
RL      Immunogenetics 44:446-452(1996).
CC      -1- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
CC      which are powerful neutrophils chemotactic factors. Binding of
CC      FMLP to the receptor causes activation of neutrophils. This
CC      response is mediated via a G-protein that activates a
CC      phosphatidylinositol-calcium second messenger system.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; X97744; CAA66328.1; -; Genomic DNA.
DR      InterPro; IPR000826; Frc/met_receptor.
DR      InterPro; IPR000276; GPCR_RHODPSIN.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00526; FMETLEUPHER.
DR      PROSITE; PR00237; GPCR_RHODOPSIN.
DR      PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR      PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW      Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor;
KW      Sensory transduction; Transducer; Transmembrane.
FT      TOPO_DOM <1 24
FT      TRANSMEM 25 47
FT      TOPO_DOM 48 58
FT      TRANSMEM 59 80
FT      TOPO_DOM 81 97
FT      TRANSMEM 98 118
FT      TOPO_DOM 119 137
FT      TRANSMEM 138 159
FT      TOPO_DOM 160 202
FT      TRANSMEM 203 223
FT      TOPO_DOM 224 239
FT      TRANSMEM 240 263
FT      TOPO_DOM 264 283
FT      TRANSMEM 284 303
FT      TOPO_DOM 304 348
FT      CARBOHYD 1 1
FT      DISULFID 95 173
FT      NON_TER 1 1
FT      SEQUENCE 348 AA; 38686 MW; E5A4D005CPA41616 CRC64;
SQ
Query Match      96.0%; Score 1744; DB 1; Length 348;
Best Local Similarity 96.6%; Pred. No. 3.5e-96;

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Matches 336; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 NFSTPLNEYEVESYASGYTVLRILPLVVLGTVFVLGNGLVIVWAGFRMTRVTTTC 63  
 1 NFSTPLNEYEVESYASGYTVLRILPLVVLGTVFVLGNGLVIVWAGFRMTRVTTTC 60

QY 64 YLNLALADFSFTATLPPLIVSMANGKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR 123  
 61 YLNLPLADFSFTATLPPLIVSMANGKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR 120

QY 124 CIGVLPVMAQNRHTVSLAMKVIVGPMILAVLTLPVPLFTVTTINGSDTYCFENFASW 183  
 121 CIGVLPVMAQNRHTVSLAMKVIVGPMILAVLTLPVPLFTVTTINGSDTYCFENFASW 180

QY 184 GGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVACYGLIAAKIHKKGMKSSRPRLRVL 243  
 181 GGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVACYGLIAAKIHKKGMKSSRPRLRVL 240

QY 244 TAVVASFFICWPFQVALLGTVWLKEMLPYGYKKIIDIIVNPTSSLAFFNSCLNPMLYV 303  
 241 TAVVASFFICWPFQVALLGTVWLKEMLPYGYKKIINIIVNPTSSLAFFNSCLNPMLYV 300

QY 304 FVGQDFRERLIRSLPTSLERALSDESAPTNDTANASAPPAETELQAM 351  
 301 FVGQDFRERLIRSLPTSLERALSDESAPTNDTANASAPPAETELQAM 348

Db

RESULT 5

PPRL1\_MACMU STANDARD; PRT; 348 AA.

ID PPRL1\_MACMU  
 AC P79190;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE FMLP-related receptor 1 (FMLP-R-1) (Fragment).  
 GN Name=PPRL1;  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopithecoidea; Cercopitheciinae; Macaca.  
 NC NCBI\_TaxID=9544;  
 RN (1)  
 NP NCBIOTIDE SEQUENCE.  
 RP MEDLINE=9642153; PubMed=8824156; DOI=10.1007/s002510050151;  
 RA Alvarez V., Coro E., Shen P., Gonzalez-Koces S., Lopez-Iarrea C.;  
 RT "Molecular evolution of the N-formyl peptide and Csa receptors in non-  
 human primates.";  
 RL Immunogenetics 44:446-452(1996).  
 CC -1- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,  
 which are powerful neutrophils chemotactic factors. Binding of  
 FMLP to the receptor causes activation of neutrophils. This  
 response is mediated via a G-protein that activates a  
 phosphatidylinositol-calcium second messenger system.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation  
 at the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.

CC EMBL: X97737; CAAG6321.1; -; Genomic\_DNA.  
 DR HSSP: P34996; 1DD.  
 DR InterPro: IPR000826; Frc/met\_receptor.  
 DR InterPro: IPR000276; GPCR\_Rhodpn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00526; FMTLEUPHER.  
 DR PRINTS: PR00237; GPCRHOPOPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KM Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor;  
 RN Sensory transduction; Transducer; Transmembrane.

FT TOPO\_DOM <1 24  
 FT TRANSLEM 25 47  
 FT TOPO\_DOM 48 58  
 FT TRANSLEM 59 80  
 FT TOPO\_DOM 81 97  
 FT TRANSLEM 98 118  
 FT TOPO\_DOM 119 137  
 FT TRANSLEM 138 159  
 FT TOPO\_DOM 160 202  
 FT TRANSLEM 203 223  
 FT TOPO\_DOM 224 239  
 FT TRANSLEM 240 263  
 FT TOPO\_DOM 264 283  
 FT TRANSLEM 284 303  
 FT TOPO\_DOM 304 348  
 FT CARBOHYD 1 1  
 FT DISULFID 95 173  
 FT NON\_TER 1 1  
 FT NON\_TER 348 348  
 SQ SEQUENCE 348 AA; 38457 MW; BC165DPAIC14B694E CRC64;

Query Match 95.8%; Score 1740; DB 1; Length 348;  
 Best Local Similarity 96.6%; Pred. No. 6e-96;  
 Matches 336; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 4 NFSTPLNEYEVESYASGYTVLRILPLVVLGTVFVLGNGLVIVWAGFRMTRVTTTC 63  
 1 NFSTPLNEYEVESYASGYTVLRILPLVVLGTVFVLGNGLVIVWAGFRMTRVTTTC 60

Db

QY 64 YLNLALADFSFTATLPPLIVSMANGKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR 123  
 61 YLNLALADFSFTATLPPLIVSMANGKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR 120

Db

QY 124 CIGVLPVMAQNRHTVSLAMKVIVGPMILAVLTLPVPLFTVTTINGSDTYCFENFASW 183  
 121 CIGVLPVMAQNRHTVSLAMKVIVGPMILAVLTLPVPLFTVTTINGSDTYCFENFASW 180

Db

QY 184 GGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVACYGLIAAKIHKKGMKSSRPRLRVL 243  
 181 GGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVACYGLIAAKIHKKGMKSSRPRLRVL 240

Db

QY 244 TAVVASFFICWPFQVALLGTVWLKEMLPYGYKKIIDIIVNPTSSLAFFNSCLNPMLYV 303  
 241 TAVVASFFICWPFQVALLGTVWLKEMLPYGYKKIINIIVNPTSSLAFFNSCLNPMLYV 300

Db

QY 304 FVGQDFRERLIRSLPTSLERALSDESAPTNDTANASAPPAETELQAM 351  
 301 FVGQDFRERLIRSLPTSLERALSDESAPTNDTANASAPPAETELQAM 348

Db

RESULT 6

088536\_MOUSE PRELIMINARY; PRT; 351 AA.

ID 088536;  
 AC 088536;  
 DT 01-NOV-1998 (TREMIREL. 08, Created)  
 DT 01-NOV-1998 (TREMIREL. 08, Last sequence update)  
 DT 01-FEB-2005 (TREMIREL. 29, Last annotation update)  
 DE N-formylpeptide receptor-like 2 (lipoxin A4 receptor-like  
 protein).  
 GN Name=fpr-ts2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NC NCBI\_TaxID=10090;  
 RN (1)  
 NP NCBIOTIDE SEQUENCE.  
 RP MEDLINE=98390190; PubMed=9722950; DOI=10.1006/geno.1998.5376;  
 RA Gao J.-L., Chen H., Fille J.D., Kozak C.A., Murphy P.M.;  
 RT "Differential expansion of the N-formylpeptide receptor gene cluster  
 in human and mouse.";  
 RL Genomics 51:270-276(1998).  
 RN (2)

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN-B10.A;  
RX MEDLINE=22206880; PubMed=12218158;  
RA Vaughn M.W., Proske R.J., Haviland D.L.;  
RT "Identification, cloning, and functional  
RT lipoxin A4 receptor homologue gene.";  
RL J. Immunol. 169:3363-3369(2002).  
RR EMBL; AF071180; AAC34585.1; -; Genomic DNA.  
DR EMBL; AY138248; AAC06932.1; -; Genomic DNA.  
DR Ensemble; ENSMG00000052270; Mus musculus.  
MG1; MGI:1278319; Pdx-rs2.  
DR GO:GO:0004872; F:receptor activity; IDA.  
DR InterPro; IPR001644; C3anrx\_receptor.  
DR InterPro; IPR000826; Fc/ret\_receptor.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7cm\_1; 1.  
DR PRINTS; PR01060; C3ANPHYLTNKR.  
DR PRINTS; PR00546; FMETLEUPHER.  
DR PRINTS; PR00237; GPCR RHODOPSIN.  
DR PROSITE; PS00237; G\_PROTEIN\_REC\_P1\_1; UNKNOWN\_1.  
DR PROSITE; PS00262; G\_PROTEIN\_REC\_P1\_2; 1.  
KM Receptor.  
SQ SEQUENCE 351 AA; 39422 MW; B16BCE7FA9A8F43 CRC64;

Query Match	78.2%	Score 1420	DB 2	Length 351
Best Local Similarity	76.3%	Pred. No. 6,6e-77		
Matches 267	Conservative 33	Mismatches 50	Indels 0	Gaps 0

  

Query	1	MEINFEPLNEXEVSYESAGYTVLRILPLVVLGVTPLVGLVGLVIVWAGFRMTRVT	60
Db	1	MEINFEPLNEXEVSYESAGYTVLRILPLVVLGVTPLVGLVGLVIVWAGFRMTRVT	60
Qy	61	TTCVNTALAAPSPFATPLPPLIVSNAMKEKPPGFLCKLHVVDINLFGSVFLIGTA	120
Db	61	TTCVNTALAAPSPFATPLPPLIVSNAMKEKPPGFLCKLHVVDINLFGSVFLIGTA	120
Qy	121	LDRCIQVLPWQAQNRHTVSLAMKIVGPMILATVLTVPVFLFTTVTIIPNGDYCTENF	180
Db	121	LDRCIQVLPWQAQNRHTVSLAMKIVGPMILATVLTVPVFLFTTVTIIPNGDYCTENF	180
Qy	181	ASWGQPEERLKVAILTMLTARGIRIFVIGFSLPMSIVAICYGLIAKIHKKMIKSRPL	240
Db	181	ASWGQPEERLKVAILTMLTARGIRIFVIGFSLPMSIVAICYGLIAKIHKKMIKSRPL	240
Qy	241	RVLTAVVASPFTCMFPFQVALLGTWMLKEMLFYCKYKIIDLVNPTSSLAFFNSCLNPM	300
Db	241	RVLTAVVASPFTCMFPFQVALLGTWMLKEMLFYCKYKIIDLVNPTSSLAFFNSCLNPM	300
Qy	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
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Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350
Db	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	350

  

Query	301	LYVAVGQDFRERLIHSLPTSLERALSBSAPLNDPAANASAPPAETELQA	35
-------	-----	---	----

RA Serhan C.N.:/

RT "Araplin-1-triggered 15-epi-lipoxin A4 (LXA4) and LXA4 stable analogues

RT are potent inhibitors of acute inflammation: evidence for anti-

RT inflammatory receptors.";

RL J. Exp. Med. 185:1693-1704(1997)..

CC -1- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,

CC which are powerful neutrophils chemotactic factors. Binding of

CC fMLP to the receptor causes activation of neutrophils. This

CC response is mediated via a G-protein that activates a

CC phosphatidylinositol-calcium second messenger system. The

CC activation of LXA4R could result in an anti-inflammatory outcome

CC connecting the actions of proinflammatory signals such as LTB4

CC (leukotriene B4).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: Expressed mostly in neutrophils, followed by

CC spleen and lung. Expressed at very low levels in heart and liver.

CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

[illegible]



QY 121 LDRGICVLHPVMAQNHRTVSLAMKVIQPMILAVLTPVPLELTVVTPINGDYCTENF 180  
 DB 121 LDRGICVLHPVMAQNHRTVSLAMKVIQPMILAVLTPVPLELTVVTPINGDYCTENF 180  
 QY 181 ASMGCTEERBLKVAITMLTARGIIRFYIGFSLPMSIYACGLIAAKIHKMKIKSRPL 240  
 DB 181 VSMGNSYBERLNTAITVTTRIGIRFYIVSPLSPMSFPAICGLITTIHKKAFNSSRPF 240  
 QY 241 RVLTAVASFFICMPFQVALLAGTVMLEKMLFYGKYKIIDILVNPSSLAFFNSCLNPM 300  
 DB 241 RVLTAVASFFICMPFQVALLAGTVMLEKMLFYGKYKIIDILVNPSSLAFFNSCLNPM 300  
 QY 301 LYVFGQDFRRLRLHSPTLSERLSDSAPNTNANSSPPMETLOQM 351  
 DB 301 LYVFGQDFRRLRLHSPTLSERLSDSAPNTNANSSPPMETLOQM 351  
 RESULT 8  
 PPR2\_HUMAN STANDARD; PRT; 353 AA.  
 AC P25089;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE FMPLP-related receptor, II (FMPLP-R-II) (Formylpeptide receptor-like 2).  
 GN Name=PPR2; Synonym=PPRHL;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
 OC Homo  
 NCBI\_TaxID=9606;  
 RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=92307681; PubMed=1612600;  
 RA Bao L., Gerard N.P., Bddy R.L. Jr., Shows T.B., Gerard C.;  
 RT "Mapping of genes for the human C5a receptor (C5AR), human FMPLP  
 receptor (PPR), and two FMPLP receptor homologue orphan receptors  
 (PPRHL, PPRH2) to chromosome 19.";  
 RL Genomics 13:437-440(1992).  
 RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=94256976; PubMed=8198572;  
 RA Durstun M., Gao J.-L., Tiliaty H.L., McDermott D., Murphy P.M.;  
 RT "Differential expression of members of the N-formylpeptide receptor  
 RT gene cluster in human phagocytes.";  
 RL Biochem. Biophys. Res. Commun. 201:174-179(1994).  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RP Kopatz S.A., Aronstam R.S., Sharma S.V.;  
 RA "cDNA clones of human proteins involved in signal transduction  
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Dege J.G.,  
 RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heide F.,  
 RA Batchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Tomblin S., Cantin P., Prange C.,  
 RA Raba S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hultk S.W.,  
 RA Vailion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Hulton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
 RA Buttefield Y.S.N., Krzywinski M.I., Skalek U., Smallins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,  
 CC which are powerful neutrophils chemotactic factors. Binding of  
 CC FMPLP to the receptor causes activation of neutrophils. This  
 CC response is mediated via a G-protein that activates a  
 CC phosphatidylinositol-calcium second messenger system.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 DR EMBL: M76673; AA58482.1; -; mRNA.  
 DR EMBL: L14061; AA52474.1; -; Genomic DNA.  
 DR EMBL: AY262690; AAP20654.1; -; Genomic DNA.  
 DR EMBL: BC059388; AAH59388.1; -; mRNA.  
 DR EMBL: BC069070; AAH69070.1; -; mRNA.  
 DR EMBL: BC069593; AAH69593.1; -; mRNA.  
 DR EMBL: BC069812; AAH69812.1; -; mRNA.  
 DR PIR: C42009; C42009.  
 DR Ensembl: ENSG00000187474; Homo sapiens.  
 DR HGN: HGNC:3828; PPR2.  
 DR MIM: 136539; -.  
 DR GO: GO:0016021; C: integral to membrane; TAS.  
 DR GO: GO:0005886; C: plasma membrane; TAS.  
 DR GO: GO:0004982; F: N-formyl peptide receptor activity; TAS.  
 DR GO: GO:0006928; P: cell motility; TAS.  
 DR GO: GO:0007165; P: signal transduction; TAS.  
 DR InterPro: IPR000826; Frl/met receptor.  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR Pfam: PF00001; 7tm\_1, 1.  
 DR PRINTS: PR00526; FMETLUPHER.  
 DR PROSITE: PR00237; GPCR\_RHOPOSN.  
 DR PROSITE: PS00237; G PROTEIN RECP F1.1; 1.  
 DR PROSITE: PS02652; G PROTEIN RECP F1.2; 1.  
 KW Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor;  
 KW Sensory transduction; Transducer; Transmembrane.  
 FT TOPO\_DOM 1 27  
 FT TRANSMEM 28 50  
 FT TOPO\_DOM 51 61  
 FT TRANSMEM 62 83  
 FT TOPO\_DOM 84 100  
 FT TRANSMEM 101 121  
 FT TOPO\_DOM 122 140  
 FT TRANSMEM 141 162  
 FT TOPO\_DOM 163 205  
 FT TRANSMEM 206 226  
 FT TOPO\_DOM 227 242  
 FT TRANSMEM 243 266  
 FT TOPO\_DOM 267 306  
 FT TRANSMEM 287 306  
 FT TOPO\_DOM 307 353  
 FT CARBOHYD 4 4  
 FT CARBOHYD 10 10  
 FT DISULFID 98 176  
 FT CONFLICT 94 94  
 FT CONFLICT 211 211  
 FT CONFLICT 338 338  
 SQ SEQUENCE 353 AA; 39965 MW; FFB150B6A833F4C CRC64;  
 Query Match 73.0%; Score 1327; DB 1; Length 353;  
 Best Local Similarity 72.2%; Pred. No. 2.3e-71;  
 Matches 225; Conservativity 38; Mismatches 58; Indels 2; Gaps 1;  
 QY 1 MERNSTPLNRYEVSYSAGTYVLRILPLVVLGTYFVVGUNGIVYVAGPRMRTY 60  
 DB 1 METNFSIPLNRYEVSYSAGTYVLRILPLVVLGTYFVVGUNGIVYVAGPRMRTY 60

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QY 61 TTYLNLALADSFATLPLPLIVSMANGKWPFGCKLHIVVDINLFGSVFLIGFIA 120
DB 61 TTYLNLALADSFATLPLPLIVSMANGKWPFGCKLHIVVDINLFGSVFLIGFIA 120
QY 121 LDRICICVLHPWAQNHRVTSAMKVIVGPWILAVLTLPVPLELTVTTIPNGDYCTCFNF 180
DB 121 LDRICICVLHPWAQNHRVTSAMKVIVGPWILAVLTLPVPLELTVTTIPNGDYCTCFNF 180
QY 181 ASWGTPPEERLKVATMTLARGIIRFVIGSLPMSIVAICYGLIAKHKKMICKSRPL 240
DB 181 ASWGTPPEERLKVATMTLARGIIRFVIGSLPMSIVAICYGLIAKHKKMICKSRPL 240
QY 241 RUTLAVASFFICWPPFQVALLGTWMLKEMLYGKKIITDILVNPSSIAFNSCLNPM 300
DB 241 RUTLAVASFFICWPPFQVALLGTWMLKEMLYGKKIITDILVNPSSIAFNSCLNPM 300
QY 301 LTVFVGODPFRRLIHSPLTSERALS--DSAPNTDPAANSASPATELQAM 351
DB 301 LTVFVGODPFRRLIHSPLTSERALS--DSAPNTDPAANSASPATELQAM 351

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## RESULT 9

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Q61534 HUMAN PRELIMINARY; PRT; 353 AA.
ID O61534
AC O61534
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE FHL2 HUMAN.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lameddin J.B., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schulze K.J., Brower A., Gordon L., Diaz J., Ramirez M.,
RA Stillwagen S., Phan H., Velasco N., Do L., Regala W., Terry A.,
RA Garner J., Danganan L., Erler A., Christensen M., Georgescu A.,
RA Avila J., Liu S., Atlix C., Andreia T., Tranheim M.,
RA Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R.,
RA Thomas P., Quan G., Krommiller B., Arellano A., Sanders C., Ow D.,
RA Nolan M., Trong S., Kobayashi A., Olsen A.S., Carraro A.V.,
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC005946; AAC72102.1; -; Genomic DNA.
SQ SEQUENCE 353 AA; 39965 MW; FFB7150B6A833F4C CRC64;

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Query Match 73.0%; Score 1327; DB 2; Length 353;

Best Local Similarity 72.2%; Pred. No. 2.3e-71;

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Matches 255; Conservative 38; Mismatches 58; Indels 2; Gaps 1;
QY 1 METNFTPLNIEYEVSYESAGYTVLRILPLVVGTVFVLGNGLVIVWAGFRMRTYT 60
DB 1 METNFTPLNIEYEVSYESAGYTVLRILPLVVGTVFVLGNGLVIVWAGFRMRTYT 60
QY 61 TTYLNLALADSFATLPLPLIVSMANGKWPFGCKLHIVVDINLFGSVFLIGFIA 120
DB 61 TTYLNLALADSFATLPLPLIVSMANGKWPFGCKLHIVVDINLFGSVFLIGFIA 120
QY 121 LDRICICVLHPWAQNHRVTSAMKVIVGPWILAVLTLPVPLELTVTTIPNGDYCTCFNF 180
DB 121 LDRICICVLHPWAQNHRVTSAMKVIVGPWILAVLTLPVPLELTVTTIPNGDYCTCFNF 180
QY 181 ASWGTPPEERLKVATMTLARGIIRFVIGSLPMSIVAICYGLIAKHKKMICKSRPL 240
DB 181 ASWGTPPEERLKVATMTLARGIIRFVIGSLPMSIVAICYGLIAKHKKMICKSRPL 240
QY 241 RUTLAVASFFICWPPFQVALLGTWMLKEMLYGKKIITDILVNPSSIAFNSCLNPM 300
DB 241 RUTLAVASFFICWPPFQVALLGTWMLKEMLYGKKIITDILVNPSSIAFNSCLNPM 300
QY 301 LTVFVGODPFRRLIHSPLTSERALS--DSAPNTDPAANSASPATELQAM 351
DB 301 LTVFVGODPFRRLIHSPLTSERALS--DSAPNTDPAANSASPATELQAM 351

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DB 301 LTVFVGODPFRRLIHSPLTSERALS--DSAPNTDPAANSASPATELQAM 353

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## RESULT 10

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O86535 MOUSE PRELIMINARY; PRT; 347 AA.
ID O86535
AC O86535
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE N-formylpeptide receptor-like 1.
GN Name=Fpr-trl;
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE:98390190; PubMed:972950; DOI=10.1006/geno.1998.5376;
RA Gao J.-L., Chen H., Fille J.D., Kozak C.A., Murphy P.M.;
RT "Differential expansion of the N-formylpeptide receptor gene cluster
in human and mouse."
RU Genomics 51:270-276(1998).
RL EMBL; AF071179; AAC34584.1; -; Genomic DNA.
DR Ensembl; ENSMUSG00000052270; Mus musculus.
DR MGI; MGI:1278320; Fpr-trl.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004982; P:N-formyl peptide receptor activity; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR001644; G3aantx_receptor.
DR InterPro; IPR000826; Frl/met_receptor.
DR InterPro; IPR000276; GPCR_rhodopsn.
DR Pfam; PF00001; 7tm1.1.
DR PRINTS; PRO1060; C3ANPHYLYXNR.
DR PRINTS; PRO0526; FMETLEUPHER.
DR PRINTS; PRO0237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_FL_2; 1.
KW Receptor.
SQ SEQUENCE 347 AA; 39071 MW; A755BF9F09575A70 CRC64;

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Query Match 72.9%; Score 1325; DB 2; Length 347;

Best Local Similarity 73.2%; Pred. No. 2.9e-71;

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Matches 257; Conservative 27; Mismatches 63; Indels 4; Gaps 1;
QY 1 METNFTPLNIEYEVSYESAGYTVLRILPLVVGTVFVLGNGLVIVWAGFRMRTYT 60
DB 1 METNFTPLNIEYEVSYESAGYTVLRILPLVVGTVFVLGNGLVIVWAGFRMRTYT 60
QY 61 TTYLNLALADSFATLPLPLIVSMANGKWPFGCKLHIVVDINLFGSVFLIGFIA 120
DB 61 TTYLNLALADSFATLPLPLIVSMANGKWPFGCKLHIVVDINLFGSVFLIGFIA 120
QY 121 LDRICICVLHPWAQNHRVTSAMKVIVGPWILAVLTLPVPLELTVTTIPNGDYCTCFNF 180
DB 121 LDRICICVLHPWAQNHRVTSAMKVIVGPWILAVLTLPVPLELTVTTIPNGDYCTCFNF 180
QY 181 ASWGTPPEERLKVATMTLARGIIRFVIGSLPMSIVAICYGLIAKHKKMICKSRPL 240
DB 181 ASWGTPPEERLKVATMTLARGIIRFVIGSLPMSIVAICYGLIAKHKKMICKSRPL 240
QY 241 RUTLAVASFFICWPPFQVALLGTWMLKEMLYGKKIITDILVNPSSIAFNSCLNPM 300
DB 241 RUTLAVASFFICWPPFQVALLGTWMLKEMLYGKKIITDILVNPSSIAFNSCLNPM 300
QY 301 LTVFVGODPFRRLIHSPLTSERALS--DSAPNTDPAANSASPATELQAM 351
DB 301 LTVFVGODPFRRLIHSPLTSERALS--DSAPNTDPAANSASPATELQAM 351

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Query Match	Best Local Similarity	Matches	Score 1312;	DB 1;	Length 349;
72.2%;	72.2%;	252;	Pred. No. 1.7e-70;	Mismatches 58;	Indels 2;
Conservative 37;	Conservative 37;	Indels 2;	Gaps 14;		

Db	1	MEINFS1P	INTEEB	LEBP	DAGH	VT	LM	IF	SL	LV	HG	TF	FG	LV	GL	YI	WA	GF	MT	IV	N	60
Qy	61	TTCY	LN	AL	AF	ST	AT	LP	EL	IV	S	M	A	G	E	K	M	F	C	M	L	61
Db	61	TTCY	LN	AL	AF	ST	AT	LP	EL	IV	S	M	A	G	E	K	M	F	C	M	L	61
Qy	121	LDRC	IC	VL	HP	WA	ON	HRT	S	LA	M	K	Y	V	G	P	M	I	A	L	121	
Db	121	LDRC	IC	VL	HP	WA	ON	HRT	S	LA	M	K	Y	V	G	P	M	I	A	L	121	
Qy	181	ASWG	T	PEER	K	VA	I	M	L	T	A	G	I	R	F	V	G	S	L	P	M	181
Db	181	ASWG	T	PEER	K	VA	I	M	L	T	A	G	I	R	F	V	G	S	L	P	M	181
Qy	241	RV	FA	VA	VS	AF	IC	MP	F	Y	I	L	I	G	A	M	A	M	L	K	E	241
Db	241	RV	FA	VA	VS	AF	IC	MP	F	Y	I	L	I	G	A	M	A	M	L	K	E	241
Qy	301	LY	VF	GD	FR	ER	L	I	H	S	L	P	T	S	L	E	R	A	L	S	E	301
Db	301	LY	VF	GD	FR	ER	L	I	H	S	L	P	T	S	L	E	R	A	L	S	E	301
RESULT 12																						
ID	FPRL2	PONPY	STANDARD	PRT	349	AA																
AC	P79237																					
DT	15-JUL-1998	(Rel. 36, Created)																				
DT	15-JUL-1998	(Rel. 36, Last sequence update)																				
DT	10-MAY-2005	(Rel. 47, Last annotation update)																				
DE	FM	LP-related receptor II (FM	LP-R-II) (Formylpeptide receptor-like 2)																			
DE	(Fragment).																					
GN	Name=FPRL2																					
OS	Pongo pygmaeus (Orangutan).																					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;																					
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;																					
OC	Pongo.																					
OX	NCBI_TaxID=9600;																					
RN	[1]																					
RP	NUCLEOTIDE SEQUENCE.																					
RX	MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;																					
RA	Alvarez V., Coto E., Shen F., Gonzalez-Koces S., Lopez-Barrea C.;																					
RT	"Molecular evolution of the N-formyl peptide and Csa receptors in non-																					
RT	human primates".																					
RL	Immunogenetics 44:446-452(1996).																					
CC	-1- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,																					
CC	which are powerful neutrophils chemotactic factors. Binding of																					
CC	FM	LP to the receptor causes activation of neutrophils. This																				



AC P79191;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE FMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like 2)  
 DE (fragment).  
 GN Name=PPRL2;  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopithecoidea; Cercopithecinae; Macaca.  
 NCBI\_TaxID=9544;  
 RX NCBIOTIDE SEQUENCE.  
 RP MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;  
 RA Alvarez V., Coto E., Sehen F., Gonzalez-Koces S., Lopez-Larrea C.;  
 RT "Molecular evolution of the N-formyl peptide and C5a receptors in non-  
 human primates.";  
 RL Immunogenetics 44:446-452(1996).  
 CC -I- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,  
 which are powerful neutrophils chemotactic factors. Binding of  
 FMLP to the receptor causes activation of neutrophils. This  
 response is mediated via a G-protein that activates a  
 phosphatidylinositol-calcium second messenger system.  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 CC EMBL: X97740; CAA66324.1; -; Genomic DNA.  
 DR InterPro: IPR000826; FRC/met\_receptor.  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00526; FMETLEUPHER.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G-PROTEIN RECP\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN RECP\_F1\_2; 1.  
 DR Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor;  
 KM Sensory transduction; Transducer; Transmembrane.  
 FT TOPO\_DOM 1 27  
 FT TRANSMEM 28 50  
 FT TOPO\_DOM 51 61  
 FT TRANSMEM 62 83  
 FT TOPO\_DOM 84 100  
 FT TRANSMEM 101 121  
 FT TOPO\_DOM 122 140  
 FT TRANSMEM 141 162  
 FT TOPO\_DOM 163 205  
 FT TRANSMEM 206 226  
 FT TOPO\_DOM 227 242  
 FT TRANSMEM 243 266  
 FT TOPO\_DOM 267 286  
 FT TRANSMEM 287 306  
 FT TOPO\_DOM 307 >349  
 FT CARBOHYD 4 4  
 FT CARBOHYD 10 10  
 FT DISULFID 98 176  
 FT NON\_TER 349 349  
 SQ SEQUENCE 349 AA; 39532 MW; CQC92A9BSCDB250C CRC64;  
 Query Match 71.1%; Score 1292; DB 1; Length 349;  
 Best Local Similarity 70.5%; Pred. No. 2,7e-69;  
 Matches 246; Conservative 39; Mismatches 62; Indels 2; Gaps 1;  
 QY 1 METNFSPLMEYREVSAGYTYTLRLPLVLYGVTVLGNGLYTVWAGPMTTYT 60  
 DB 1 METNFSPLMEYREVSAGYTYTLRLPLVLYGVTVLGNGLYTVWAGPMTTYT 60  
 QY 61 TICVNLALADPFSPTATLPLIVSMANGKWPFGMFLCKLIHIVVDINLFGSVPLIGFIA 120

DB 61 TICVNLALADPFSPTATLPLIVSMANGKWPFGMFLCKLIHIVVDINLFGSVPLIGFIA 120  
 QY 121 LDRICICVLPVPMQONRTVSLAMKIVGPMIALVTLPLFPLFTVTPNGDYTFNF 180  
 DB 121 LDRICICVLPVPMQONRTVSLAMKIVGPMIALVTLPLFPLFTVTPNGDYTFNF 180  
 QY 181 ASWGTPEERLKYAITMLTARGIIRFVIGFSLMSIVAICYGLIAKHKKIKSRPL 240  
 DB 181 PFWGDFVVERMNVFITMAKVSILHFIIGFSPMSIITWCYGIIVAKIKRMTKSRPL 240  
 QY 241 RUTANVASPFICWPPQVALLGTWLMKMLFYGKXKIIDIVNPTSSLAFFNSCLNPM 300  
 DB 241 HITAVASFFICWPPQVALLGTWLMKMLFYGKXKIIDIVNPTSSLAFFNSCLNPM 300  
 QY 301 LYYFVQODPRRLIHSPLTSERALSE--DSAPNTNANSAPPAETE 347  
 DB 301 LYYFVQODPRRLIHSPLTSERALTEVDSQTSNHTTSASPPETE 349  
 RESULT 15  
 PPRL\_HUMAN STANDARD; PRT; 350 AA.  
 AC P21462; Q14939; Q726A4; Q86U52; Q9NS48;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE fMet-Ileu-Phe receptor (FMLP receptor) (N-formyl peptide receptor)  
 DE (PPR) (N-formylpeptide chemotactant receptor).  
 GN Name=PPRL;  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RX NCBIOTIDE SEQUENCE.  
 RP MEDLINE=90267449; PubMed=2161213;  
 RA Boulay F., Tardif M., Brouchon L., Vignais P.;  
 RT "Synthesis and use of a novel N-formyl peptide derivative to isolate a  
 human N-formyl peptide receptor cDNA.";  
 RL Biochem. Biophys. Res. Commun. 168:1103-1109(1990).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=91105045; PubMed=2176894;  
 RA Boulay F., Tardif M., Brouchon L., Vignais P.;  
 RT "The human N-formylpeptide receptor. Characterization of two cDNA  
 isolates and evidence for a new subfamily of G-protein-coupled  
 receptors.";  
 RL Biochemistry 29:11123-11133(1990).  
 RN [3]  
 RN NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=91286286; PubMed=1712023;  
 RA Murphy P.M., McDermott D.;  
 RT "Functional expression of the human formyl peptide receptor in Xenopus  
 oocytes requires a complementary human factor.";  
 RL J. Biol. Chem. 266:12560-12567(1991).  
 RN [4]  
 RN NUCLEOTIDE SEQUENCE.  
 RX PubMed=1612600;  
 RA Bao L., Gerard N.P., Eddy R.L. Jr., Shows T.B., Gerard C.;  
 RT "Cloning of genes for the human C5a receptor (C5AR), human FMLP  
 receptor (PPR), and two FMLP receptor homologue orphan receptors  
 (PPRH1, PPRH2) to chromosome 19.";  
 RL Genomics 13:437-440(1992).  
 RN [5]  
 RN NUCLEOTIDE SEQUENCE.  
 RA Perez H.D.;  
 RN Submitted (MAR-1993) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RN NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=94040825; PubMed=8224916; DOI=10.1016/0378-1119(93)90653-K;  
 RA Murphy P.M., Tiffany H.L., McDermott D., Ahuja S.K.;

```

RT "sequence and organization of the human N-formyl peptide receptor-
RL encoding gene."
RT Gene 133:285-290(1993).
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANTS VAL-101; LYS-192
RP AND GLU-346.
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Gutrice CDNA resource center (www.cdna.org).";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS VAL-101 AND GLU-346.
RA Kalnina N., Chen X., Rolfe A., Hallack A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labber J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) system donor
RT vector."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15057824; DOI=10.1038/nature02399;
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branncomb E.,
RA Cenepeel S., Carrano A.V., Cault C., Chan Y.M., Christensen M.,
RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Deter J.C.,
RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,
RA Ghalavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
RA Hayda L., Ho I., Huang W., Izant S., Jett J., Kadner K., Kimball H.,
RA Kobayashi A., Lartionov D., Leem S.-H., Lopez F., Lou Y., Lowry S.,
RA Melfatti S., Martinez V., McCready P.M., Medina C., Morgan J.,
RA Nelson K., Nolan M., Ovcharenko I., Piatuck S., Pollard M.,
RA Podjke A.P., Predki P., Qian G., Ramirez L., Rash S., Reiter J.,
RA Rodriguez A., Rogers S., Salamon A., Salazar A., She X., Smith D.,
RA Slezak T., Solovayev V., Thayer N., Tice H., Tse H., Tsai M., Ustaszewski A.,
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
RA Purey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
RA Pennecchio L.A., Richardson P., Stubbs L., Kohner D.S., Myers R.M.,
RA Rubin E.M., Lucas S.M.;
RT "The DNA sequence and biology of human chromosome 19."
RL Nature 428:529-535(2004).
RN [10]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA MEDLINE=22388257; Feingold E.A., Grouse L.H., Derge J.G.,
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tohyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaralle P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywnicki M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [11]
RP NUCLEOTIDE SEQUENCE OF 1-5.
RX PubMed=144895;
RA Perez H.D., Holmes R., Kelly E., McClary J., Chou Q., Andrews W.H.;
RT "Cloning of the gene coding for a human receptor for formyl peptides.
RT Characterization of a promoter region and evidence for polymorphic
RT expression."

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RL Biochemistry 31:11595-11599(1992).
RN [12]
RP PHOSPHORYLATION SITES SER-328; THR-329; THR-331; SER-332; THR-334;
RP THR-336; SER-338 AND THR-339.
RX MEDLINE=99445530; PubMed=10514456; DOI=10.1074/jbc.274.42.29791;
RA Meesters D.C., Potter R.M., Prosenitz E.R.;
RT "Differential phosphorylation paradigms dictate desensitization and
RT internalization of the N-formyl peptide receptor."
RL J. Biol. Chem. 274:29791-29795(1999).
CC -1- FUNCTION: High affinity receptor for N-formyl-methionyl peptides,
CC which are powerful neutrophils chemotactic factors. Binding of
CC fMLP to the receptor causes activation of neutrophils. This
CC response is mediated via a G-protein that activates a
CC phosphatidylinositol-calcium second messenger system.
CC -1- TISSUE SPECIFICITY: Neutrophils.
CC -1- PFM: Phosphorylated; which is necessary for desensitization.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, M37128; AAA36362.1; -; mRNA.
DR EMBL, M60626; AAA35846.1; -; mRNA.
DR EMBL, M60627; AAA35847.1; -; mRNA.
DR EMBL, L10820; AAA1863.1; -; Unassigned DNA.
DR EMBL, AY301273; AAP58403.1; -; Genomic DNA.
DR EMBL, BC007429; AAP58403.1; -; mRNA.
DR EMBL, AC018755; AAF87842.1; -; Genomic DNA.
DR EMBL, BC005315; AAH05315.1; -; mRNA.
DR EMBL, S49810; AAD14906.1; -; mRNA.
DR PIR, JC2014; A42009.
DR Ensembl: ENSG00000171051, Homo sapiens.
DR HGNCG, HGNC:3826; PPRI.
DR H-InvDB, HIX0015389; -.
DR MIM, 136537; -.
DR GO, GO:0005768; C:cytosol; TAS.
DR GO, GO:0016021; C:integral to membrane; TAS.
DR GO, GO:0005886; C:plasma membrane; TAS.
DR GO, GO:0004982; F:N-formyl peptide receptor activity; TAS.
DR GO, GO:0004872; F:receptor activity; TAS.
DR GO, GO:0000187; P:activation of MAPK; TAS.
DR GO, GO:0006928; P:cell motility; TAS.
DR GO, GO:0006935; P:chemotaxis; TAS.
DR GO, GO:0007186; P:G-protein coupled receptor protein signaln. ; TAS.
DR GO, GO:0007188; P:G-protein signaling, coupled to GPCR; TAS.
DR GO, GO:0007263; P:intracellular signal transduction; TAS.
DR GO, GO:0007165; P:signal transduction; TAS.
DR InterPro, IPR000826; FcR/met receptor.
DR InterPro, IPR000276; GPCR_Rhodopsn.
DR Pfam, PR00001; 7tm 1; 1.
DR PRINTS, PR00526; FMTLEUPHER.
DR PRINTS, PR00237; GPCR_Rhodopsn.
DR PROSITE, PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE, PS00262; G_PROTEIN_RECPT_F1_2; 1.
DR Chemotaxis; G-protein coupled receptor; Glycoprotein; Phosphorylation;
DR Polymorphism; Receptor; Sensory transduction; Transducer;
DR Transmembrane.
KW TOPO DOM 1 27
KW TOPO DOM 28 50
KW TOPO DOM 51 61
KW TOPO DOM 62 83
KW TOPO DOM 84 100
KW TOPO DOM 101 121
KW TOPO DOM 122 140
KW TOPO DOM 141 162
KW TOPO DOM 163 205
KW TOPO DOM 206 226
KW TOPO DOM 227 242
KW TOPO DOM 243 266

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FT	TOPO_DOM	267	285	Extracellular (Potential).
FT	TRANSMEM	286	305	7 (Potential).
FT	TOPO_DOM	306	350	Cytoplasmic (Potential).

FT	TOPO_DOM	267	285	Extracellular (Potential).
FT	TRANSMEM	286	305	7 (Potential).
FT	TOPO_DOM	306	350	Cytoplasmic (Potential).

FT	TOPO_DOM	267	285	Extracellular (Potential).
FT	TRANSMEM	286	305	7 (Potential).
FT	TOPO_DOM	306	350	Cytoplasmic (Potential).

Query Match	68.4%;	Score 1243.5;	DB 1;	Length 350;
Best Local Similarity	68.6%;	Prod No. 2 19-66.		

Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;

Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;

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Qy 61 TTYCYLNTALADESFATLPPLIVSNAMGKWPGEWLCRLIHIVDINTFGSVLLGFIA 120
Db 61 TTYSLNTALAVADPCFSTLPFPFMYVRKAMGHWPGWLCRFLPIIVDINTFGSVFLIALIA 120
Qy 121 LDRCTCVLHPVWAQXNHRITVSLANKVIVGFWIILALVTLPEFLFTVTIIPNGDTCTFNF 180
Db 121 LDRCCVCLHPVWTQXNHRITVSLAKKVIIGFWVMALLTLPELIRVTIVPGKTGVACTCFNF 180
Qy 181 ASWGTPPEBRKVALTYMLTARGIIRVIVGFSLPMSVVALCYGLIAKIKHKKGIKSSRPL 240
Db 181 SPMTNDPPEKRIINVAAMLRVIRGIIRFIIIGFSAPMSVVAVSYGLIARKIKHOGIKSSRPL 240
Qy 241 RVLTAIVVASPFICWFPBPOLVALIGTWMLKEMLFYGYKYLIDILVNPTSSIAFPNSCLNPM 300
Db 241 RVLSTVVAALAFPLCWSBPYQVVALIATVRIEEL-OGMYKIRIGLAVDVTSAALAFNSCLNPM 299
Qy 301 LVYFVGODFRERLISHLPSTLERALSQDSQAPNTDITLANSASPAAETELQA 350
Db 300 LVYFVGODFRERLIALPASTLERALTEDSTQISDTATNSTLPEAEVALQA 349

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Qy 61 TICYLNLALADESFATLPPLIVSNAMGKWPGEWLCRLIHIVDINTFGSVLLGFIA 120
Db 61 TISYLNLAADVADPCFSTLPFPFMYRKAMGHWPGWLCRFLPIIVDINLFGSVFLIALIA 120
Qy 121 LDRICIYVHPVWAQXNHRITVSLANKVIVGFWIILALVITLPEFLFTVTIIPNGDYCTENF 180
Db 121 LDRICVYHPVWTQXNHRITVSLAKKVIIGFWVMALITLPEIIRVTVIPGKTGVACTENF 180
Qy 181 ASWGTPPEBRKVALTYMLTARGIIRVIVGFSLPMSVVALCYGLIAKIKHKKGIKSSRPL 240
Db 181 SPMTNDPPEKRIINVAAMLRVGIIRFIIIGFSAPMSVVAVSYGLIARKIKHOGIKSSRPL 240
Qy 241 RVLTAIVVASPFICWFPBPOLVALIGTWMLKEMLFYGYKYLIDILVNPTSSIAFPNSCLNPM 300
Db 241 RVLSTVVAALAFPLCWSBPYQVVALIATVRIEEL-OGMYKIIIGLAVDVTSAALAFNSCLNPM 299
Qy 301 LYVPFGODFRERLIIHSLPTSELRALSQDSQAPNTNDTAAANSAPPAETELQA 350
Db 300 LYVPFGODFRERLIIHALPASLBERALTEDBTQISDITANSTLPEALVATLQA 349

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Qy 61 TICYLNLALADESFATLPPLIVSNAMGKWPGEWLCRLIHIVDINTFGSVLLGFIA 120
Db 61 TISYLNLAADVADPCFISTLPFPFMYRKAMGHWPGWLCRFLPIIVDINLFGSVFLIALIA 120
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Db 121 LDRICVYHPVWTQXNHRITVSLAKKVIIGFWVMALITLPEIIRVTVIPGKTGVACTENF 180
Qy 181 ASWGTPPEBRKVALTYMLTARGIIRVIVGFSLPMSVVALCYGLIAKIKHKKGIKSSRPL 240
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QY      61 TICYLNALADESFATPLPPLIVSNAMGEKWPGEMLCKLIHVVDINTFGSVLLGFIA 120
Db      61 TISYLNTLAADVPCFTSTLPFPFWVRKMGHMPGWGLCKFLPIIYDINLFGSVFLIALIA 120
QY      121 LDRICI CVLHPWAQNHRITS LANKVIVGEMIALALVTLPEFLFTVTIIPNGDTCTENF 180
Db      121 LDRICVCLHPVWTQNNRITVSLAKKVIIIGVMVALLTLPILIRVTTVPKGTGVACTCFNF 180
QY      181 ASWGTPBEERKLVAITTMLTARGIIRVIVGFSLPMSGVALCYGLIAKKIKKGKIKSRPL 240
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[illegible][illegible]

Search completed: March 28, 2006, 13:20:00  
Job time : 279.992 secs

**Job time : 279.992 secs**

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2006, 13:20:18 ; Search time 62.712 Seconds  
(without alignments)  
462.737 Million cell updates/sec

Title: US-10-517-956-1

Perfect score: 1817  
Sequence: 1 METNFTPLNXYEVSYSAGY...TNDTANASAPPAETELQAM 351

Scoring table: BLOSUM62  
Gapco 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1817	100.0	351	2	US-09-944-807-2
2	1811	99.7	351	2	US-09-826-509-501
3	1244.5	68.5	350	2	US-09-826-509-499
4	1243.5	68.4	350	1	US-07-759-568-3
5	1240.5	68.3	350	2	US-08-430-286A-8
6	1174.5	64.6	364	1	US-08-458-970A-10
7	1117	61.5	315	1	US-08-118-270-34
8	1117	61.5	315	4	PCT-US93-08528-34
9	626.5	34.5	125	2	US-08-513-974B-348
10	524.5	30.5	356	2	US-09-170-496D-246
11	553.5	30.5	356	2	US-09-170-496D-270
12	513	28.2	350	1	US-08-458-970A-9
13	509.5	28.0	482	2	US-09-117-440-2
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16	506.5	27.9	482	2	US-09-826-509-465
17	504.5	27.8	395	2	US-08-981-825-6
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19	499	27.5	355	2	US-09-170-496D-2
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22	479	26.4	304	4	PCT-US93-08528-35
23	464	25.5	124	2	US-08-513-974B-349
24	447	24.6	126	2	US-08-513-974B-350
25	426.5	23.5	355	1	US-07-759-568-1
26	426.5	23.5	355	1	US-08-450-393A-8
27	426.5	23.5	355	1	US-08-390-000A-5

28	426.5	23.5	355	2	US-08-446-669-8	Sequence 8, Appl1
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30	426.5	23.5	355	4	PCT-US95-00476-8	Sequence 8, Appl1
31	426.5	23.5	359	1	US-08-458-970A-11	Sequence 11, Appl1
32	426.5	23.5	358	1	US-08-148-209A-4	Sequence 4, Appl1
33	426.5	23.5	359	2	US-09-867-915-3	Sequence 3, Appl1
34	426.5	23.5	360	1	US-08-202-056-7	Sequence 7, Appl1
35	426.5	23.5	360	2	US-09-409-778-4	Sequence 4, Appl1
36	426.5	23.5	381	2	US-09-949-016-7391	Sequence 7391, Ap
37	426.5	23.5	381	2	US-09-949-016-7392	Sequence 7392, Ap
38	426.5	23.5	383	2	US-09-949-016-7115	Sequence 7115, Ap
39	426.5	23.5	383	2	US-08-153-848-46	Sequence 46, Appl
40	419.5	23.1	337	1	US-08-299-843A-46	Sequence 46, Appl
41	419.5	23.1	337	2	US-09-088-337B-46	Sequence 46, Appl
42	419.5	23.1	337	4	PCT-US93-11153-46	Sequence 46, Appl
43	419.5	23.1	352	1	US-08-202-056-3	Sequence 3, Appl1
44	419.5	23.1	352	1	US-08-076-093A-4	Sequence 4, Appl1
45	419.5	23.1	352	1	US-08-076-093A-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1  
US-09-944-807-2  
Sequence 2, Application US/09944807  
Patent No. 6773895  
GENERAL INFORMATION:  
APPLICANT: Boehringer Ingelheim Pharma KG  
TITLE OF INVENTION: Method for identifying substances which positively influence inflammatory conditions of chronic  
TITLE OF INVENTION: Inflammatory airway diseases  
FILE REFERENCE: 082.00n  
CURRENT APPLICATION NUMBER: US/09/944,807  
CURRENT FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: UK 0021484.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 2  
LENGTH: 351  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-944-807-2

Query Match	100.0%	Score 1817	DB 2	Length 351
Best Local Similarity	100.0%	Pred. No. 9.5e-127		
Matches 351	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	METNFTPLNXYEVSYSAGYTVLRILPLVVLGVTVGVVGLVGLVIVVAGFRMTRTYT	60	
DB	1	METNFTPLNXYEVSYSAGYTVLRILPLVVLGVTVGVVGLVGLVIVVAGFRMTRTYT	60	
QY	61	TTCTYLMALADSFSTTLPPLIVSNAMGKMPGWLCKLHIVDINFGSVFLIGFLA	120	
DB	61	TTCTYLMALADSFSTTLPPLIVSNAMGKMPGWLCKLHIVDINFGSVFLIGFLA	120	
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DB	181	ASWGTPEERLKVATIMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIKKMKISRP	240	
QY	241	RVTAVVASFFICWPFQVALIGTWLKMFLYKIKYIIDIIVNPTSSLAFFNSCLNPM	300	
DB	241	RVTAVVASFFICWPFQVALIGTWLKMFLYKIKYIIDIIVNPTSSLAFFNSCLNPM	300	
QY	301	LVYFVQDREPRIRHSLPTSLBRALSEDAPTNDTANASAPPAETELQAM	351	
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RESULT 2
US-09-826-509-501
; Sequence 501, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Brulinema, Karin
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patentin Version 2.1
; SEQ ID NO 501
; LENGTH: 351
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-826-509-501

Query Match          99.7%; Score 1811; DB 2; Length 351;
Best Local Similarity 99.7%; Pred. No. 2.6e-126;
Matches 350; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 METNFSPLNEXBEVSYESAGYVLRLLPLVLTGTFVLGNGLVYVWAGFRMTRTYT 60
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DB 61 TICYLNLALADSFPTATLPFLIVSMAMGKMPFGMFLCKLHIVDINLFGSVFLIGFTA 120
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DB 121 LDRICVLHPVMAQNHRVTSIAKVIIGVPIIALVLTLPVFLFTVTTIPNGDTYCTFNF 180
QY 181 ASWGGTPEERLKVATIMLTARGIIRFVIGFSLPMSIYAIYGLIAAKIHKKMIKSSRPL 240
DB 181 ASWGGTPEERLKVATIMLTARGIIRFVIGFSLPMSIYAIYGLIAAKIHKKMIKSSRPL 240
QY 241 RVLTAVASFFICWPFQVALIGTWLKKMLFYGKYKIIDILVNPSSIAFPNSCLNPM 300
DB 241 RVLTAVASFFICWPFQVALIGTWLKKMLFYGKYKIIDILVNPSSIAFPNSCLNPM 300
QY 301 LVYFVGODFRERLIHSLPTSLERALSSEDSAPTNDTANASAPPAETELQAM 351
DB 301 LVYFVGODFRERLIHSLPTSLERALSSEDSAPTNDTANASAPPAETELQAM 351

RESULT 3
US-09-826-509-499
; Sequence 499, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Brulinema, Karin
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
```

```
; SOFTWARE: Patentin Version 2.1
; SEQ ID NO 499
; LENGTH: 350
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-826-509-499

Query Match          68.5%; Score 1244.5; DB 2; Length 350;
Best Local Similarity 68.6%; Pred. No. 1.7e-84;
Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;

QY 1 METNFSPLNEXBEVSYESAGYVLRLLPLVLTGTFVLGNGLVYVWAGFRMTRTYT 60
DB 1 METNFSPLNEXBEVSYESAGYVLRLLPLVLTGTFVLGNGLVYVWAGFRMTRTYT 60
QY 61 TICYLNLALADSFPTATLPFLIVSMAMGKMPFGMFLCKLHIVDINLFGSVFLIGFTA 120
DB 61 TICYLNLALADSFPTATLPFLIVSMAMGKMPFGMFLCKLHIVDINLFGSVFLIGFTA 120
QY 121 LDRICVLHPVMAQNHRVTSIAKVIIGVPIIALVLTLPVFLFTVTTIPNGDTYCTFNF 180
DB 121 LDRICVLHPVMAQNHRVTSIAKVIIGVPIIALVLTLPVFLFTVTTIPNGDTYCTFNF 180
QY 181 ASWGGTPEERLKVATIMLTARGIIRFVIGFSLPMSIYAIYGLIAAKIHKKMIKSSRPL 240
DB 181 ASWGGTPEERLKVATIMLTARGIIRFVIGFSLPMSIYAIYGLIAAKIHKKMIKSSRPL 240
QY 241 RVLTAVASFFICWPFQVALIGTWLKKMLFYGKYKIIDILVNPSSIAFPNSCLNPM 300
DB 241 RVLTAVASFFICWPFQVALIGTWLKKMLFYGKYKIIDILVNPSSIAFPNSCLNPM 300
QY 301 LVYFVGODFRERLIHSLPTSLERALSSEDSAPTNDTANASAPPAETELQAM 350
DB 301 LVYFVGODFRERLIHSLPTSLERALSSEDSAPTNDTANASAPPAETELQAM 349
```

```
RESULT 4
US-07-759-568-3
; Sequence 3, Application US/07759568
; Patent No. 5374506
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
; TITLE OF INVENTION: Human Interleukin-8 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,568
; FILING DATE: 19910913
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELETYPE: 6714627 cush
; INFORMATION FOR SEQ ID NO. 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: AMINO ACID
```

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-759-568-3

Query Match 68.4%; Score 1243.5; DB 1; Length 350;  
Best Local Similarity 68.6%; Pred. No. 2.1e-84;  
Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;

QY 1 METNFTPLNEBESVESAGYTVLRILPLVVLGTVLGVNGVIVVAGFRMTRTVT 60  
DB 1 METNFTPLNEBESVESAGYTVLRILPLVVLGTVLGVNGVIVVAGFRMTRTVT 60  
QY 61 TICVLMALADPSFTATLPFLIVSMANGKMPGKFLKLIHIVDINLFGSVFLIGFIA 120  
DB 61 TICVLMALADPSFTATLPFLIVSMANGKMPGKFLKLIHIVDINLFGSVFLIGFIA 120  
QY 121 LDRICVHLHPVNAQNRTVSLAMKVIIGPMIALVLTLPFLVTITPNSGTYCTFNF 180  
DB 121 LDRICVHLHPVNAQNRTVSLAMKVIIGPMIALVLTLPFLVTITPNSGTYCTFNF 180  
QY 181 ASWGTPEERLKYAITMLTARGIIRFVIGSLPMSIYVACGLIAKIHKKMIKSSRPL 240  
DB 181 SPWTNDPKERIKYAVAMLTVRGIIRFVIGSLPMSIYVACGLIAKIHKKMIKSSRPL 240  
QY 241 RVLTAVASFPICMPFEOVALLGTVLWKEMLFYGYKIIDILVNPTSSLAPFNSCLNPM 300  
DB 241 RVLTAVASFPICMPFEOVALLGTVLWKEMLFYGYKIIDILVNPTSSLAPFNSCLNPM 300  
QY 241 RVLSFVAAPFLCWSYQVALATVIRIELL-QGMYKEIGIADVTSALAFNSCLNPM 299  
QY 301 LYFVQODFERRLIHSPTSLERALSSEDSPNTDPAANSASPAETELQA 350  
DB 301 LYFVQODFERRLIHSPTSLERALSSEDSPNTDPAANSASPAETELQA 350

RESULT 5  
US-08-430-286A-8  
Sequence 8, Application US/08430286A

GENERAL INFORMATION:  
PATENT No. 6225080  
APPLICANT: Unl, George R.  
APPLICANT: Eppier, C. Mark  
APPLICANT: Wang, Jai-Bel  
TITLE OF INVENTION: Mu-Subtype Opioid Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: US  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,286A  
FILING DATE: 28-APR-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Robinsen, Joseph R.  
REGISTRATION NUMBER: 33,448  
REFERENCE/DOCKET NUMBER: 0646/1A843-US5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: P-REP  
US-08-430-286A-8

Query Match 68.3%; Score 1240.5; DB 2; Length 350;  
Best Local Similarity 68.6%; Pred. No. 3.4e-84;  
Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;

QY 1 METNFTPLNEBESVESAGYTVLRILPLVVLGTVLGVNGVIVVAGFRMTRTVT 60  
DB 1 METNFTPLNEBESVESAGYTVLRILPLVVLGTVLGVNGVIVVAGFRMTRTVT 60  
QY 61 TICVLMALADPSFTATLPFLIVSMANGKMPGKFLKLIHIVDINLFGSVFLIGFIA 120  
DB 61 TICVLMALADPSFTATLPFLIVSMANGKMPGKFLKLIHIVDINLFGSVFLIGFIA 120  
QY 121 LDRICVHLHPVNAQNRTVSLAMKVIIGPMIALVLTLPFLVTITPNSGTYCTFNF 180  
DB 121 LDRICVHLHPVNAQNRTVSLAMKVIIGPMIALVLTLPFLVTITPNSGTYCTFNF 180  
QY 181 ASWGTPEERLKYAITMLTARGIIRFVIGSLPMSIYVACGLIAKIHKKMIKSSRPL 240  
DB 181 SPWTNDPKERIKYAVAMLTVRGIIRFVIGSLPMSIYVACGLIAKIHKKMIKSSRPL 240  
QY 241 RVLTAVASFPICMPFEOVALLGTVLWKEMLFYGYKIIDILVNPTSSLAPFNSCLNPM 300  
DB 241 RVLTAVASFPICMPFEOVALLGTVLWKEMLFYGYKIIDILVNPTSSLAPFNSCLNPM 300  
QY 241 RVLSFVAAPFLCWSYQVALATVIRIELL-QGMYKEIGIADVTSALAFNSCLNPM 299  
QY 301 LYFVQODFERRLIHSPTSLERALSSEDSPNTDPAANSASPAETELQA 350  
DB 301 LYFVQODFERRLIHSPTSLERALSSEDSPNTDPAANSASPAETELQA 350

RESULT 6

US-08-458-970A-10  
Sequence 10, Application US/08458970A

GENERAL INFORMATION:  
PATENT No. 5861272  
APPLICANT: LI, ET AL.  
TITLE OF INVENTION: C5a Receptor  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,970A  
FILING DATE: June 2, 1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 364 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: 1linear  
MOLECULE TYPE: protein  
US-08-458-970A-10

Query Match 64.6%; Score 1174.5; DB 1; Length 364;  
Best Local Similarity 64.6%; Pred. No. 2,7e-79;  
Matches 237; Conservative 38; Mismatches 73; Indels 19; Gaps 5;

1 MENTFSTPLNBYE-----EVSYSAGTVLRILPLVVLGYTPVLGVNGLVIMVAG 52  
1 MDTNMSLLMKKSAVNIMNVSSTQSVSAGYIVDVESYILFAVTFVLGVNGLVIMVAG 60  
53 FRRTFRTVTTTCYANLALADFSFTATLPPLIVSNAMGKMPFGNLCGLIHIVDILFGS 112  
61 FRKHTVTTTISYANLALADFCFTSTLPFIASVMGGMFGMCKCFITVTDILNFGS 120  
113 VFLIGFIALDRICVLAHPVMAQNHRTVSLAMKVIYGVWIALVLTLPVLELTVTTPN- 171  
121 VFILIALDRICVLAHPVMAQNHRTVSLAKKVIYVWICAPILTLPVIRLTTV--PNS 178  
172 ----GDTTCFNPASNGTPEERLKAVALTMLTARGIIRFVIGFSLPMSIVATCYGLIAK 227  
179 RLGPGRITACTFDFSPPTKQVEERKVAVMTLVRGIIIRFIIIGFSTPMIVATCYGLITTK 238  
228 IHKGMIKSRPLRVLTAVVASFFICMFPQVALLGTVMLEKMLFGYKKIIDIIVNPT 287  
239 IHOGILKSRPLRVLSFVVAALFLLCKPCFQVALLSTIOVRRLKMPFGIYVTL-KIT 297  
288 SSIAFNSCLNPMLYVFGQDFRERLIHSIPTSLEKALSASAPNTDAN--SASPPA 344  
298 SPLAFNSCLNPMLYVFGQDFRERLIHSIPTSLEKALSASAPNTDAN--SASPPA 357  
QY 345 ETELOAM 351  
DB 358 ENTINAM 364

RESULT 7  
US-08-118-270-34  
Sequence 34, Application US/08118270  
GENERAL INFORMATION:  
APPLICANT: Murphy, Randall B.  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/118,270  
FILING DATE: 09-SEP-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY-2A

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 315 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: 1linear  
MOLECULE TYPE: peptide  
US-08-118-270-34

Query Match 61.5%; Score 1117; DB 1; Length 315;  
Best Local Similarity 67.3%; Pred. No. 4.1e-75;  
Matches 218; Conservative 37; Mismatches 59; Indels 10; Gaps 4;

QY 27 ILPLVVLGYTPVLGVNGLVIMVAGFRMTFRTVTTTCYANLALADFSFTATLPPLIVSMA 86  
1 IITVFAVRFVLGVNGLVIMVAGFRMTHTVTTTISYANLALADFCFTSTLPFPMVRLG 60  
QY 87 MGEKMPFGNLCGLIHIVDILNFGSVFLIGFIALDRICVLAHPVMAQNHRTVSLAMKVI 146  
61 ---HMPFGNLCGLIHIVDILNFGSVFLIALDRICVLAHPVMAQNHRTVSLAKKVI 117  
QY 147 VGPWIALVLTLPVPLFTVTTPINGDITCTNFPASGCTPEERLKAVALTMLTARGIIRF 206  
118 IGPWVWIALVLTLPVIRIYIVPGKTGYVACTNFPMTNDPERINVAVALTVGILRF 177  
QY 207 VIGFSLPMSIVATCYGLIAKIHKKGMIKSRPLRVLTAVVASFFICMFPQVALLGTV 266  
178 IIGFSLPMSIVATCYGLIAKIHKKGMIKSRPLRVLSFVVAALFLLCKPCFQVALLSTIOVRRLKMPFGIYVTL-KIT 232  
QY 267 WKEMLFGYKKIIDIIVNPTSSIAFNSCLNPMLYVFGQDFRERLIHSIPTSLEKALS 326  
233 RIRELL-QGMYEKIGIAVDVTSALAFNSCLNP-LYVFGQDFRERLIHSIPTSLEKALS 290  
QY 327 EDSAPNTDANASASAPATELOA 350  
DB 291 EDSQTSTATNTSTLPSAEVALQA 314

RESULT 8  
PCT-US93-08528-34  
Sequence 34, Application PC/TUS9308528  
GENERAL INFORMATION:  
APPLICANT: New York University  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08528  
FILING DATE: 09-SEP-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT  
TELECOMMUNICATION INFORMATION:

RESULT 9  
 US-08-513-974B-348  
 Sequence 348, Application US/08513974B  
 Patent No. 6114139  
 GENERAL INFORMATION:  
 APPLICANT: Hinuma, Shuji  
 APPLICANT: Hosoya, Masaki  
 APPLICANT: Fujii, Ryo  
 APPLICANT: Ohtaki, Teiuya  
 APPLICANT: Fukushima, Shoji  
 APPLICANT: Ohbi, Kazuhiro  
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN  
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
 NUMBER OF SEQUENCES: 380  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0., Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/513,974B  
 FILING DATE: 14-SEP-1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP95/01599

```

Query Match          34.5%; Score 626.5; DB 2; length 125;
Best Local Similarity 99.2%; Pred. No. 2, 6e-39;
Matches 124; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      125  ICVLHPVAQNHRTVSLMKVIVGPMILALVTLPLPFLPLTYYTIRNGDYYCTPNFASWG 184
        |||
Db       1  ICVLHPVAQNHRTVSLMKVIVGPMILALVTLPLPFLPLTYYTIRNGDYYCTPNFASWG 60

QY      185  GTPPERLKVAT-MLTARGIIRFVIGFSLPMSIVAICYGHLIAKHKKGMKSSRPRLV 243
        |||
Db       61  GTPPERLKVATIMLTARGIIRFVIGFSLPMSIVAICYGHLIAKHKKGMKSSRPRLV 120

QY      244  TAVVA 248
        |||
Db       121 TAVVA 125

RESULT 10
US-09-170-496D-246
; Sequence 246, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Law, Chen W
; TITLE OF INVENTION: NO. 6555339-Endogenous, Constitutively Activated Human G Protein-c-
```

```

; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 246
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-246

```

Query Match 30.5%; Score 554.5; DB 2; Length 356;

Best Local Similarity 41.0%; Pred. No. 1.5e-33; Matches 126; Conservative 59; Mismatches 113; Indels 9; Gaps 4;

```

QY 25 LRLPLVAVLGTVFVLGNGLVIVWAGFPMRTVTTCYLANLADFSFTATLP---FL 81
DB 42 LRLPLVAVLGTVFVLGNGLVIVWAGFPMRTVTTCYLANLADFSFTATLP---FL 81
QY 82 IYSMANGKMPFGWFLCKLHIIVDINLFGSVFLIGFIALDRICIYLAHPVMAQNHRTVSL 141
DB 102 IYS-----RQWLDEBMACCKLITTFVFLSYFASNCLLVFISVDRICISVLVPWALNHRIVQR 157
QY 142 AMKVIYGPMLALVLTLPVFLPTTITPNGDTYCTFPNPSMGSTPEERLKAITMLTAR 201
DB 158 ASWLAFGVWLAAALCSAHLKFRITRKW-NGCTHCYLAFNSDNETAQIMEGVEGHIIG 216
QY 202 GILRFVIGFSLPMSIYVACGYLAAKIHKKGMIKSSRPLRVLTAVVAFPICWFPQOLVA 261
DB 217 TIGHFLGFLGFLAIGTCAHLIRAKLIREGWVHAKRPKLLVLSAFTFMSPPNVV- 275
QY 262 LIGTVALKEMLPYKKYKIIDILVNPTSSLAFFNSCLNPMLYVFGODFRERLIHSLPTSL 321
DB 276 LVVHLMRVRVWLKRIYHPRMLLIIQASFALGCVNSSLNPLFYVFGVGRDFQEKFGSLTSL 335
QY 322 ERALSED 328
DB 336 ARAFGEE 342

```

## RESULT 11

```

US-09-170-496D-270
; Sequence 270, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 270
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-270

```

Query Match 30.5%; Score 553.5; DB 2; Length 356;

Best Local Similarity 41.0%; Pred. No. 1.8e-33; Matches 126; Conservative 59; Mismatches 113; Indels 9; Gaps 4;

```

QY 25 LRLPLVAVLGTVFVLGNGLVIVWAGFPMRTVTTCYLANLADFSFTATLP---FL 81
DB 42 LRLPLVAVLGTVFVLGNGLVIVWAGFPMRTVTTCYLANLADFSFTATLP---FL 81
QY 82 IYSMANGKMPFGWFLCKLHIIVDINLFGSVFLIGFIALDRICIYLAHPVMAQNHRTVSL 141
DB 102 IYS-----RQWLDEBMACCKLITTFVFLSYFASNCLLVFISVDRICISVLVPWALNHRIVQR 157

```

```

QY 142 AMKVIYGPMLALVLTLPVFLPTTITPNGDTYCTFPNPSMGSTPEERLKAITMLTAR 201
DB 158 ASWLAFGVWLAAALCSAHLKFRITRKW-NGCTHCYLAFNSDNETAQIMEGVEGHIIG 216
QY 202 GILRFVIGFSLPMSIYVACGYLAAKIHKKGMIKSSRPLRVLTAVVAFPICWFPQOLVA 261
DB 217 TIGHFLGFLGFLAIGTCAHLIRAKLIREGWVHAKRPKLLVLSAFTFMSPPNVV- 275
QY 262 LIGTVALKEMLPYKKYKIIDILVNPTSSLAFFNSCLNPMLYVFGODFRERLIHSLPTSL 321
DB 276 LVVHLMRVRVWLKRIYHPRMLLIIQASFALGCVNSSLNPLFYVFGVGRDFQEKFGSLTSL 335
QY 322 ERALSED 328
DB 336 ARAFGEE 342

```

## RESULT 12

```

US-08-458-970A-9
; Sequence 9, Application US/08458970A
; Patent No. 5861272
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: C5a Receptor
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSER: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,970A
; FILING DATE: June 2, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09234
; FILING DATE: 16 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1744
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-970A-9

```

Query Match 28.2%; Score 513; DB 1; Length 350;

Best Local Similarity 33.6%; Pred. No. 1.8e-30; Matches 122; Conservative 60; Mismatches 129; Indels 52; Gaps 9;

```

QY 4 NSTP-LMEYER-----VSYSAGTYVLRIPLVVLGTVFVLGNGLVIVWAGF 53
DB 5 NNTTDPYGHYDDKDTLDINTPVDKTSNTLRVPDIALVIFAVVFLVGLGNALVWVWTA 64
QY 54 RMTRTVTTCYLANLADFSFTATLPPLIVSMANGKMPFGWFLCKLHIIVDINLFGSV 113
DB 65 EAKRTIINAIWFLNADFLSCLALPILFTSIVQHHNPFQGAACSIILPSILILNNYASI 124

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QY 114 FLIGFIALDRICICVLHPVNAQNRHTVSLANKVIWGPWILALVLTLPVFLPTVTIENG 173  
| | | | | : : : : : | | | | | : : : : :  
Db 125 LILATISADRFLLVPRKICWQNRGAGLAVIACVAMGLALLTLTISFLVRV-----RE 179  
QY 174 TY-----CTFNASMGCTPEERLKAVALTMLRGIRFVIGSLPMSIYAICGLIAK 227  
| | | | | : : : : : | | | | | : : : : :  
Db 180 EYPPPKVLCGVDSH-----DKRRERAV-----AIVRLVGLFWPLTLTICYTEFLLR 228  
QY 228 IHKKGMIKSRPLRVLTAVVASFICWFPOLVALLGTWVKEMLFYGYKKIIDILVNP 287  
| | | | | : : : : : | | | | | : : : : :  
Db 229 TMSRRATRSKTKLVAVVAVASFIFLWLYQVTGIM-----MSFLBSSPTFLIAKL 281  
QY 288 SSL-----AFPNSCINPMLVYFVGODPRERLIHSLPTSLERLSEDSR-----PTND 334  
| | | | | : : : : : | | | | | : : : : :  
Db 282 DSLCVFAYINCCINPIIYVAVAGFGGRLKSLPLSLRVLNVEESVVRKSFTSTVD 341  
QY 335 TAA 337  
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Db 342 TWA 344

RESULT 13  
US-09-117-440-2  
; Sequence 2, Application US/09117440  
; Patent No. 6521418  
; GENERAL INFORMATION:  
; APPLICANT: Ye, Richard D  
; TITLE OF INVENTION: A G PROTEIN-COUPLED RECEPTOR WITH AN ENLARGED  
; FILE REFERENCE: SCR2041S  
; CURRENT APPLICATION NUMBER: US/09/117,440  
; EARLIER FILING DATE: 1998-07-28  
; EARLIER APPLICATION NUMBER: PCT/US97/01736  
; EARLIER FILING DATE: 1997-01-30  
; EARLIER APPLICATION NUMBER: 60/010,808  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO: 2  
; LENGTH: 482  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-117-440-2

Query Match 28.0%; Score 509.5; DB 2; Length 482;  
Best Local Similarity 26.6%; Pred. No. 4,4e-30;  
Matches 134; Conservative 59; Mismatches 117; Indels 193; Gaps 11;  
QY 2 ETN-----FSTPLNXYEBSYBSAGYTVLRILPLVVLGVTFVLGVLGNGLVIVVAGFRMTR 57  
| | | | | : : : : : | | | | | : : : : :  
Db 7 ETNSTDLISQPNNEPPV-----ILSNVILSLTFLDLPLRGVLVWVAGLKMQR 54  
QY 58 TTTTICYNLALADSFATLPLPLIVSMAMGKMPGWLCKLHIIVDINLFGSVFLIG 117  
| | | | | : : : : : | | | | | : : : : :  
Db 55 TVNTIWFHLTLADLCLSLPFSIAHLALQGMYPGRFLCKLIPSIIVLNMFAVFLTL 114  
QY 118 FILDPRICICVLHVVNAQNRHTVSLANKVIWGPWILALVLTLPVFLPTVTIENGDTYCT 177  
| | | | | : : : : : | | | | | : : : : :  
Db 115 AISLDRLCLVFKPIWQNRHNVGMACSIGCIWVAVFWCMIPVYVRELIPTTDNHR-CG 173  
QY 178 FNEA-----SW----- 183  
| | | | | : : : : : | | | | | : : : : :  
Db 174 YKFGSSSLDYPDPYGDPLENRSLENIIVORFGEMNDRLSDSSQTDNDHPTVTVFQPR 223  
QY 184 -----GGTPEE-----R 190  
Db 234 FGRPSADSLPRGSARLTSQLYSGNFKPADVVSFKIPSGPRIDHETSPLDNGDAFLSTH 293  
QY 191 LKV-----AITMLTAGIIRFVIGFSLPMSIYA 218  
| | | | | : : : : : | | | | | : : : : :  
Db 294 LKLFPSASNSFYESBLPGGFODYVNLGPTDDOVPTPLVALITITRLVVGFLPSVIMI 353

QY 219 ICYGLIAIKIHKKMIKS-SRPLRVLTAVVASFICWFPOLVALLGTWVKEMLFYGYK 277  
| | | | | : : : : : | | | | | : : : : :  
Db 354 ACYSFVFRMORGRFAKSQKTFRVAVVAVVAVFLVCMTEYHI-----F 396  
QY 278 KIIDLINPTS-----SLAFNSCINPMLVYFVGODPRERLIHSLPTSLER 323  
| | | | | : : : : : | | | | | : : : : :  
Db 397 GVSLTLDPTDPTGLKTMMSWDHVCIALMASNCFNFFLALIGKDRKAROSIIGILBA 456  
QY 324 ALSED-----SAPYNDTANSAS 341  
| | | | | : : : : : | | | | | : : : : :  
Db 457 APSEELTRSTHCPNSNVISERN 479

RESULT 14  
US-08-876-874-2  
; Sequence 2, Application US/08876874  
; Patent No. 5942405  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert  
; APPLICANT: Bergsma, Derek  
; APPLICANT: Foley, James  
; APPLICANT: Kumar, Chandrika  
; APPLICANT: Sarau, Henry  
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING  
; TITLE OF INVENTION: METHODS USING C3A RECEPTOR AND C3A  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/876,874  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/019,627  
; FILING DATE: 16-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: P50501  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 482 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULAR TYPE: protein  
; US-08-876-874-2

Query Match 28.0%; Score 508.5; DB 1; Length 482;  
Best Local Similarity 26.6%; Pred. No. 5.2e-30;  
Matches 134; Conservative 59; Mismatches 117; Indels 193; Gaps 11;  
QY 2 ETN-----FSTPLNXYEBSYBSAGYTVLRILPLVVLGVTFVLGVLGNGLVIVVAGFRMTR 57  
| | | | | : : : : : | | | | | : : : : :  
Db 7 ETNSTDLISQPNNEPPV-----ILSNVILSLTFLDLPLRGVLVWVAGLKMQR 54  
QY 58 TTTTICYNLALADSFATLPLPLIVSMAMGKMPGWLCKLHIIVDINLFGSVFLIG 117  
| | | | | : : : : : | | | | | : : : : :  
Db 55 TVNTIWFHLTLADLCLSLPFSIAHLALQGMYPGRFLCKLIPSIIVLNMFAVFLTL 114

QY 118 FIALDRICICVLHPVMAQNHRTVSLAMKVIQVPMILALVTLVPFLFTVTITINGDTYCT 177  
 DB 115 A1SLDRCLVFKPIWQNHRTVMAQSIICGCIWVAVCMCIPIVAVREIPTDNHR-CG 173  
 QY 178 FNA-----SW----- 183  
 DB 174 YKGLSSSLDYPDYGDPLENRSLNIWPPGEMNDLDSFQTDHPMTVPTVPOPT 233  
 QY 184 -----GTPRE-----R 190  
 DB 234 FQRPASDLSLRGSAKLTSQNLVSNVFKPADVSPKIPSGPIEDHESPLDNGDALFSTH 293  
 QY 191 LKV-----ATMLTARGIIRFVIGFSLPMSTVA 218  
 DB 294 LKLPFPAASNSFYESLPGQFQDYVNLGQFTDDQVPTPLVALTRLVVGFLLPSVIMI 353  
 QY 219 ICGGLAAKHKHGMKKS-SRPLRVLTAVVASFICFPQVALLGTWLEKMLFYGKT 277  
 DB 354 ACYSFIVFRQGRFAKSQKTRFVAVVAVVAVLCWTPYHI-----F 396  
 QY 278 KIIDIIVNPTS-----SLAFNSCLNPMLYVGVGDFRERLIHSLPTSLER 323  
 DB 397 GVLSLTDPETPLGKTLMSWDHVCIALASANSQFNPLVALLKDRKKAKOSIQGILEA 456  
 QY 324 ALSED-----SAPTNDTAANSAS 341  
 DB 457 AFSEELTRSTHCPSSNNVISERNIS 479

RESULT 15  
 US-09-826-509-467  
 / Sequence 467, Application US/09826509  
 / Patent No. 6806054  
 / GENERAL INFORMATION:  
 / APPLICANT: Lehmann-Bruhnsma, Karin  
 / APPLICANT: Liaw, Chen W.  
 / TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G  
 / TITLE OF INVENTION: Protein-Coupled Receptors  
 / FILE REFERENCE: AREN-207  
 / CURRENT APPLICATION NUMBER: US/09/826,509  
 / CURRENT FILING DATE: 2001-04-05  
 / PRIOR APPLICATION NUMBER: 60/195,747  
 / PRIOR FILING DATE: 2000-04-07  
 / PRIOR APPLICATION NUMBER: 09/170,496  
 / PRIOR FILING DATE: 1998-10-13  
 / NUMBER OF SEQ ID NOS: 589  
 / SOFTWARE: Patent Version 2.1  
 / SEQ ID NO 467  
 / LENGTH: 350  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-09-826-509-467

Query Match 27.9%; Score 507; DB 2; Length 350;  
 Best Local Similarity 33.3%; Pred. No. 4.9e-30;  
 Matches 121; Conservative 60; Mismatches 130; Indels 52; Gaps 9;

QY 4 NSTP-LNRYEE-----VYESAGTYVLRILPLVVLGVTFLVGLNGLVIVVAGF 53  
 DB 5 NYTPDYGHYDDDTLDLNTPTVDKTSNTLRVPDILALVFAVFLVGLGNALVWVWTA 64  
 QY 54 RMTRTVTTCYVNLALADPSFTATLPFLIVSMAMGEKMPGWFGLCKLIHVVDINFGSV 113  
 DB 65 EAKRTINAIWFLNALAVADFLSCIALPILFTSIQHHMPGAGACSLPSLIILNNYASI 124  
 QY 114 FLIGFIALDRICICVLHPVMAQNHRTVSLAMKVIQVPMILALVTLVPFLFTVTITINGD 173  
 DB 125 LILATISADRPILVFPKIQNHRTVMAQSIICGCIWVAVCMCIPIVAVREIPTDNHR-CG 173  
 QY 174 TY-----CTNFPASGSGTPEERLKVATIMLTARGIIRFVIGFSLPMSTVAICYGLIAAK 227

DB 180 EYFPKVLGVDYSH-----DKRREAV-----AIVRLVGLFPLMLTLTITCTYPIILR 228  
 QY 228 IHKGMKSSRLPLRVLTAVVASFICFPQVALLGTWLEKMLFYGKYKIIDIIVNPT 287  
 DB 229 TWSRATRTSTKTKVAVVAVVASFIFMLPYQTGIM-----MSFLBSSPTPLINKL 281  
 QY 288 SSL-----AFNSCLNPMLYVGVGDFRERLIHSLPTSLERALSEDA-----PTWD 334  
 DB 282 DSLCVSFAYINCINPIIYVAGQGFQGRLRKSLPSLLNNVLTEBSVVRSSKSPTRSTVD 341  
 QY 335 TAA 337  
 DB 342 TMA 344

Search completed: March 28, 2006, 13:22:08  
 Job time : 63.712 secs